PTO-1590 (1-2000)

SEARCH REQUEST FORM clandificand free mical bin formation Center

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Requester's Full Name: KAREN	A CANELLA	Examiner # : 776.87	Date: 8/28	6/
Art Unit: 1642 Phone N	umber 308-8-362	_ Serial Number: _ <i>6</i> ்	1503,089	<u>}</u>
Mail Box and Bldg/Room Location: $SE/2$	8D \$ 3 Resul	ts Format Preferred (circle	PAPER DISK	E-MAIL
If more than one search is submit	tted, please prioritize	searches in order of in	ieed. ********	*****
Please provide a detailed statement of the s				
Include the elected species or structures, ke utility of the invention. Define any terms of known. Please attach a copy of the cover sh	hat may have a special mea	ning. Give examples or releva		
	See .			
Title of Invention:			(h)	
Inventors (please provide full names):			70	<u> </u>
	1 months			
Earlies Priority Filing Date:		_		gerill.
For Sequence Searches Only* Please include appropriate serial number.	all pertinent information (p	arent, child, divisional, or issued	patent numbers) along	vith the
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(D) 5EQ	ID NO:4			
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Searcher / / / / / Searcher	Type of Search	vendors and cost	where applicable	o de la companya de
Searcher Phone # 3300 /570 /570	AA' Sequence (#)	Dialog	The second of the second	Andrew Comments
Searcher Location: Butter Oil -	Structure (#)	Questel/Orbit		
Date Searcher Picked Up: 8/28/07	Bibliographic	Dr.Link		
Date Completed	Litigation	Lexis/Nexis		<u> </u>
Searcher Prep & Review Time:	Fulltext	Sequence Systems ABSS	52	
Clerical Prep Time:	Patent Family	WWW/Internet	11.9 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1 1.1	
Online Time: 3	Other	Other (specify)		

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Minimum DB
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Perfect score:
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/cgn2_6/ptodata/2/paa/USO8_COMB.pep:*
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/cgn2_6/ptodata/2/paa/USO85_COMB.pep:*
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/cgn2_6/ptodata/2/paa/USO86_COMB.pep:*
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19 US-09-503-089A-5
10 US-09-655-272-5
5 US-09-144-914-5
8 US-09-436-265-5
2 US-08-816-0112-62
2 US-08-816-011-62
2 US-08-816-011-55
2 US-08-816-011-55
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ALIGNMENTS

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APPLICANT: Lessge, Florian
APPLICANT: Fink, Michel
APPLICANT: Fink, Michel
APPLICANT: Fink, Michel
APPLICANT: Fink, Michel
APPLICANT: Family OF MAMMALIAN POTASS (My CHA)
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY K THE
FILE REFERENCE: 989.67.05CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER FILING DATE: 1996-10-15
EARLIER FILING DATE: 1996-04
EARLIER FILING DATE: 1996-09-04
EARLIER FILING DATE: 1996-09-01
SEQ ID NOS: 24
SOFTWARE: PATENTING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTING DATE: 1996-02-08
SEQ ID NO 4
LENGTH: 394
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
FOTHER INFORMATION: TASK
US-09-144-914-4
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US-09-144-914-4
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Query Match
Best Local Similarity
Matches 394; Conserv

Conservative

100.0%; Score 2042; i. 100.0%; Pred. No. 1.^. tive 0; Mismatches

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Indels Length 394;

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Gaps

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APPLICANT: LEGAME, ELOMANN
APPLICANT: SALINAS, MIGUEL
APPLICANT: SALINAS, MIGUEL
APPLICANT: LAZDUNGKI, MICHEL
APPLICANT: LAZDUNGKI, MICHEL
TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THE
TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCRE
TITLE OF INVENTION: DRUGS
FILE REFERENCE: 1201-CIP2-00
CURRENT APPLICATION NUMBER: US/09/436,265
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1996-11-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 394
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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GENERAL INFORMATION:
APPLICANT: REYES, ROBERTO
APPLICANT: DUPRAT, FABRICE
APPLICANT: DUPRAT, FABRICE
                                                                                                                 Query Match 100.0%; Score 2042; DB 18; Best Local Similarity 100.0%; Pred. No. 1.9e-197; Matches 394; Conservative 0; Mismatches 0;
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OTHER INFORMATION:
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GENERAL INFORMATION:
APPLICANT: PATEL, AMANDA J.
APPLICANT: HONORE, ERIC
APPLICANT: HONORE, FLORTAN
APPLICANT: LESAGE, FLORTAN
APPLICANT: LAZDUSKI, MICHEL
TITLE OF INVENTION: A method for the identific; on FILE REFERENCE: f17b2prov3-humanTREK
CURRENT APPLICATION NUMBER: US/09/503,089A
CURRENT ETLING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Word 2000
SEQ ID NO 5
LENGTH: 394
TYPE: PRT
ORGANISM: Mus sp.
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; OTHER INFORMATION:
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US-09-503-089A-5
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CURRENT FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: PCT/FR99/00404

PRIOR FILING DATE: 1999-02-23

PRIOR APPLICATION NUMBER: FR 98/02725

PRIOR FILING DATE: 1998-03-05

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 394
RESULT 5
US-09-144-914-5
; Sequence 5, Application US/09144914;
; GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: LESAGE, FLORIAN
APPLICANT: LESAGE, FLORIAN
APPLICANT: DUPRAT, FABRICE
TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM C
TITLE OF INVENTION: OCTIVATABLE BY POLYUNSATURATED FATTY
TITLE OF INVENTION: OF SAID CHANNELS IN DRUG SCREENING
FILE REFERENCE: 1383-00
CURRENT APPLICATION NUMBER: US/09/655,272
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ORGANISM: Unknown
FEATURE:
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APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASS: UN CHR
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY ://R THE
FILE REFERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144.914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749.816
EARLIER FILING DATE: 1996-11-15
EARLIER FILING DATE: 1996-11-15
EARLIER FILING DATE: 1996-01-03
EARLIER APPLICATION NUMBER: 60/095,234
EARLIER APPLICATION NUMBER: FR 96/01565
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US-09-436-265-5
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                                                                                                                                                                                                 Sequence 5, Application US/09436265
GENERAL INFORMATION:
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Best Local S
APPLICANT: REYES, ROBERTO
APPLICANT: LESAGE, FLORIAN
APPLICANT: LESAGE, FLORIAN
APPLICANT: LESAGE, FLORIAN
APPLICANT: FINK, MICHEL
APPLICANT: SALINAS, MICHEL
APPLICANT: FARMAN, NICOLETTE
APPLICANT: LAZDUNSKI, MICHEL
TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: DRUGS
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APPLICANT: Lesage, Flor
APPLICANT: Fink, Michel
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357; Conserv
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Pred. No. 7.
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CURRENT APPLICATION NUMBER: US/09/436,265
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1998-08-04
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/107,692
PRIOR FILING DATE: 1996-11-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 405
TYPE: PRT
ORGANISM: Murine sp.
OTHER INFORMATION: TASK
US-09-436-265-5
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GENERAL INFORMATION:
APPLICANT: Pausch, Mark H
APPLICANT: Price, Laura A
                                SEQ ID NO 55
LENGTH: 309
TYPE: PRT
ORGANISM: Mus musculus
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Best Local Similarity
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TITLE OF INVENTION: POTASSIUM CHANNELS, NUCI
TITLE OF INVENTION: AND METHODS OF USING SI
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011C
CURRENT FILING DATE: 1997-03-11
                                                                                     PRIOR APPLICATION NUMBER: 08/332,312
PRIOR FILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.1
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88.1%;
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Pred. No. 7.6e-175;
9; Mismatches 25;
                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCES ENCODING
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US-08-816-011C-62
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SOFTWARE: PatentIn Ver.
SEQ ID NO 62
LENGTH: 309
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Best Local Similarity
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APPLICANT: PRICE, LAURA A
APPLICANT: PRICE, LAURA A
APPLICANT: PRICE, LAURA A
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: AND METHODS OF USING SAME
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011C
CURRENT FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: 08/332,312
PRIOR APPLICATION NUMBER: 08/332,312
PRIOR PILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 64
COLUMN NUMBER: 04 1
242 VVLREMTMNAEDEKRDAEHRALLTRNGQAGGGGG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 WTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVA::\--SCTSSRAHGHRRFLNL 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVASA SCTSSRAHGHRRFLNL
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Pred. No. 6.7€
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                                                ....GSAHTTDTASSTAAA 291
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/816,011 FILING DATE: 11-MAR-1997 CLASSIFICATION: 536
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CITY: Parsippany
CTATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-683-2134
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Price, Laura A. APPLICANT: Pausch, Mark H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-SOFTWARE.
310 A 310
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                                                                                                                                        193
                                                                                                                                                     181 YEHWTEFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIG--AF 238
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                                                                                                                                                                                                                        121 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
                                                                                                     239
                                                                                                                                                                                                                                                                             73 RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFCMFYALLGIPL 132
                                                                                                                                                                                                                                                                                             64 RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKV---FCMFYALLGIPL 120
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STRANDEDNESS: sir
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                              13 ENVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLELRARYNLSEGGYEELE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                   LNLVVLRFMTMNAEDEKRDAEHRALLTHNGQAVGLGGLSCLSGSLGDGVRPRDPVTCAAA
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                                                                                                                                    YERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVASA---SCTSSRAHGHRRF
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Encoding Them, and Methods of Using Same
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83.1%;
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Pred. No. 9.9e-115;
8; Mismatches 27;
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RESULT 11
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US-08-816-011A-55
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Best Local Similarity 83.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                          181 YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIG--AF 238
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                                                                                                                                                                                             291 A 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 11-MAR-1997 CLASSIFICATION: 536
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201-683-4117
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Pred. No. 9.9e-
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Sequence 2, Application US/09516279

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Sequence 4, Application US/09516279
GENERAL INFORMATION:
APPLICANT: David M. Duckworth
APPLICANT: Robert J. Godden
APPLICANT: Conrad G. Chapman
APPLICANT: Helen J. Meadows
TITLE OF INVENTION: MOYEL COMPOUNDS
FILE REFERENCE: GP-30200
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Best Local Similarity
Matches 233; Conserv
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APPLICANT: David M. Duckworth
             CURRENT APPLICATION NUMBER: US/09/516,279
CURRENT FILING DATE: 2000-03-01
EARLIER APPLICATION NUMBER: UK 9905061.9
EARLIER FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: UK 0003112.0
EARLIER FILING DATE: 2000-02-09
NUMBER OF SED ID NOS: 4
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CURRENT FILING DATE: 2000-03-01
EARLIER APPLICATION NUMBER: UK 9905061.9
EARLIER FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: UK 0003112.0
EARLIER APPLICATION NUMBER: UK 0003112.0
EARLIER FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
  SOFTWARE:
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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30200
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Вb Qy

Query Match Best Local S

Matches

Local Similarity hes 233; Conserv

54.7%;

Score 1116; DB 13: Pred. No. 1.1e-324; Mismatches 44-4

Length 374;

Gaps

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1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIEROEÅJ..RQQELRARYNLSOGGYE 60

MKRQNVRTLSLIVCTFTYLLVGAAVFDALESDHEMREEEKLKAEEIRIKGKYNISSEDYR

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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7472584CD1
US-60-199-020-2
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-516-279-4
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US-60-199-020-2
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; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRT
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LENGTH: 374
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APPLICANT: Nguyen, Danniel B.
APPLICANT: Policky, Jennifer L.
TITLE OF INVENTION: TRANSPORTERS AND ION
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                                                                                                                                                  CURRENT APPLICATION NUMBER: US/60/199,020
CURRENT FILING DATE: 2000-04-20
NUMBER OF SEQ ID NOS: 4
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                                                                                                                                                                                                      FILE REFERENCE: PI-0073 P
                                                                   ORGANISM: Homo sapiens
                                                     FEATURE:
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59.0%;
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Pred. No. 1.1e-103;
4; Mismatches 9;
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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-518-866-5
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GENERAL INFORMATION:
APPLICANT: Curtis, Rory J
APPLICANT: Glucksmann, Maria A
TITLE OF INVENTION: A NOVEL POTASSIUM CHANNEL MOLECULE AND USES THEREFOR
FILE REFERENCE: MNI-093
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Best Local Similarity
Matches 167; Conserv
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                                                                                 FEGWTFFHAYYYCFITLTTIGFGDFVALQSGEALQRKLPYVAFSFLYILLGLTVIGAFLN
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Search completed: August 28, Job time: 604 sec

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RESULT 15 US-09-518-866-2

Sequence 2, Application US/09518866 GENERAL INFORMATION:

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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 400 .
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Best Local Similarity
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APPLICANT: Glucksmann, Maria A
TITLE OF INVENTION: A NOVEL POTASSIUM CHANNEL FOR ECULE
FILE REFERENCE: MNI-093
CURRENT APPLICATION NUMBER: US/09/518,866
CURRENT FILING DATE: 2000-03-03
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LVVLRFLVASADWPERAA
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2: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
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Copyright (c) 1993 - 2000 Compugen
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     Sequence 15, Appli Sequence 1, Appli Sequence 1, Appli Sequence 59, Appli Sequence 22, Appli Sequence 22, Appli Sequence 81, Appli Sequence 81, Appli Sequence 81, Appli Sequence 11, Appli Sequence 11, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 2, Appli Sequence 5, Appli Sequence 6, Appli Sequence 20, Appli Sequence 6, Appli Sequence 6, Appli Sequence 20, Appli Sequence 20, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, 
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APPLICANT: Powers, Scott
APPLICANT: Powers, Scott
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCNB: A NOVel Potassium
FILE REFERENCE: 0.18781-004010US
CURRENT APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 394
TYPE: PRT
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FEATURE:
OTHER INFORMATION: human potassium
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US-60-304-243-9
US-60-309-378-2
US-60-309-378-2
US-09-760-469-1
US-09-760-469-1
US-09-73-655A
US-60-299-378-7
US-09-372-422A
US-60-304-243-1
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Result

Minimum Maximum

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9': Indels

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Length 374;

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286

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GENERAL INFORMATION: Novel proteins and Nucleic Aci.
FILE OF INVENTION: Novel proteins and Nucleic Aci.
FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USN 60/171,329
PRIOR APPLICATION NUMBER: USN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61
SEQ ID NO 61
TYPE: PRT
ORGANISM: Mus musculus
US-09-746-491-61
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                                                                      SEQ ID NO 1
LENGTH: 374
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Best Local Similarity
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APPLICANT: Powers, Scott
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCNB: A Novel Potassium Channel Protein
FILE REFERENCE: 018781-004010US
CURRENT APPLICATION NUMBER: US/09/798,584.
CURRENT FILING DATE: 2001-03-03
                                                                                                                        PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
                                                                                                         SOFTWARE: PatentIn Ver. 2.1
FEATURE:
OTHER INFORMATION: human KCNB (Potassium Channel
                                   ORGANISM: Homo sapiens
                                                          TYPE: PRT
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96.1%;
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US-09-746-491-60
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Matches
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SOFTWARE: PatentIn Ver.
SEQ ID NO 60
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Best Local Similarity
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CURRENT FILLING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
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TITLE OF INVENTION: Novel Proteins and Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 15966-621
                                                                                                                                                                                                                                                                                                                                          LENGTH: 365
TYPE: PRT
ORGANISM: Cavia porcellus
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                                                    TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANWVL.::FFSC1STLCIGAAAFSH 180
                                                                                                                                                                       YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVA.:SEVYILTGLTVIGAFLN
                                   TLVMFQSLGERMNTFVRYLLKRIKKCCGMRNTEVSMENMV!/3FFSCMGTLCIGAAAFSQ 180
                                                                                                                                      ELERVYLRLKPHKAGVQWRFAGSFYFAITVITTIGYGH/ PSTDGGKVFCMFYALLGIPL 120
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59.0%;
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No. 3.9e-93
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US-09-746-491-59

Sequence 59, Application US/09746491

GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
FILE REFERENCE: 1596-621

CURRENT APPLICATION NOWEL Proteins and Nucleic Acids Enc.
FILE REFERENCE: 1596-621

CURRENT APPLICATION NUMBER: US/09/746,491

CURRENT FILING DATE: 2000-12-20

PRIOR APPLICATION NUMBER: USSN 60/171,329

PRIOR FILING DATE: 1999-12-21

NUMBER OF SEQ ID NOS: 72

SOFTWARE: Patentin Ver. 2.0
                                                                                                                 US-09-746-491-58
; Sequence 58 Application US/09746491
; GENERAL INFORMATION:
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Best Local Similarity
Matches 167; Conserv
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LENGTH: 330
            CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
                                                                        APPLICANT: Burgess, Catherine E. TITLE OF INVENTION: Novel Proteins and Nucleic Acids FILE REFERENCE: 15966-621
NUMBER OF
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                                                                                                                                                                                                                    LVVLRFLVASADWPERAA
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ID NOS:
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NAME/KEY: VARIANT
LOCATION: (340)
OTHER INFORMATION: Wherein Xaa is any
OTHER INFORMATION: specification
US-09-746-491-22
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US-09-746-491-22
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Matches
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LENGTH: 330
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 2000-12-20
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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US-09-336-643-83
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                                                             Sequence 2, Application US/09431367B
GENERAL INFORMATION:
APPLICANT: CUITIS, ROTY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
FILE REFERENCE: MNI-074CP
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GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
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SOFTWARE: FastSEQ for
SEQ ID NO 83
LENCTH: 411
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Best Local :
          CURRENT APPLICATION NUMBER: US/09/431,367B CURRENT FILING DATE: 1999-11-01 PRIOR APPLICATION NUMBER: 09/259,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/336,643
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR APPLICATION NUMBER: PCT/US99/03826
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                                                                                                                                                                                                                                                          217
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wes 91; Conserv
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                                                                                                                                                                                                                                                  QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTRN 267
                                                                                                                                                                                                                                                                                                          FCIIYALLGIPLFGFLLAGVGDQLGTIF-----GKGIAKVEDTFIKWNVSQTKIRI 208
                                                                                                                                                                                                                                                                                                                                                                                                                            ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                     ISTITFILFGCVLFVALPATIFKHIEGWSALDATYFVVITLTTIGFGDYVAGGSD--IEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 411;
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SEQ ID NO 8
LENGTH: 313
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Best Local Similarity
Matches 90; Conserv
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Best Local (
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TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
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                                                                                                           YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCY: C:LDAFVERVLAAG---RLG 73
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                                                                                           -ANMVLIGFFSCISTLC-- 172
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                                                         ACMHLVALLGVVVTVCFL 186
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Indels Length 313;

59;

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187

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; LENGTH: 313
; TYPE: PRT
; ORGANISM: H.
US-09-336-643-81
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; Sequence 5, Application US/09431367B
; GENERAL INFORMATION:
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SEQ ID NO 81
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Best Local
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CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR PPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
                                    CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
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                                                                                                            APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES
FILE REFERENCE: MNI-074CP
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APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: NOVEL Human Potassium Channels
FILE REFERENCE: SEQ-15P
                     NUMBER OF
                                                                                                                                                                                                                                                                                                        243 FLGLVAMVLVLQTFRHVSDLHGLTELILLPPPCPASFNADEDDR 286
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                                                                                                                                                                                                                                                                                                                                                                                                                             IGAAAFSHYEH-WTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQ---YVAFSFVYI 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TMLLLTASAQRLSLL---LTHVPLSWLSMRWGWDPRRA----ACWHLVALLGVVVVTVCFL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVVLRLKPHKAGVQ---WRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RVVLANASGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPT 133
                     SEQ ID NOS: 12
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LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-11
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US-09-431-367B-11
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Best Local Similarity
Thas 76; Conserv
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Best Local
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TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
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                                      221 ISAEELPGPKLGTCPSRPSCSMELFERSHALEKQNTLQL: AMERSNSCPELVLGRLSY 280
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Local Similarity 22.9%;
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                                                                                                                      MFLVLTDTGDILATILSTSYNRFRKFPFFTRPLLSKWCF VI JKKKPDPKPADEAVPQII 220
                                                                                                                                                            TLVMFQSLGERINTLVRYLLHRAKK------
                                                                                                                                                                                                QGHLQKVKPQWENRTTHWSFLSSLFFCCTVFSTVGYGY'
                                                                                                                                                                                                                                ERVVLRLKPH--KAGVQWRFAGSFYFAITVITTIGYGH, J. DGGKVFCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                   LCFLCFLVTYALVGAVVFSAIEDGQVLVAADDGEFEKFL;
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GLGMRRADVSMANMVLI--GFFSCISTLCT : AFSHYE-HWTFFQAYYYC 193
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29.9%; Pred. No. 4.9e-
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Pred. No. 4.7e-15:

39; Mismatches 16; Indels 129;
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Matches

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US-09-760-469-1386, Application US/09760469
; Sequence 1386, Application US/09760469
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ54
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US-09-746-491-63
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APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic
FILE REFERENCE: 15966-621
                                                                                                                                                                                                                                                                                                                                                               Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1983
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1386
LENGTH: 205
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 39
TYPE: PRT
                                                                                                                                                                                                                                          Query Match
Best Local 9
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Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
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|:||||||| | : | :||: |: || | :
335 FVTLTTIGFGDTVL-----EHPNFFLFFSIYIIVGMEIVFIAFKLVQNRLI 380
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                                  256 RDAEH 260
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                                                                                                                                               42
                                                                                                                                                                                                                                          Local Similarity
EDQVH 161
                                                                      PGEGYNQKFREL----YKIGITCYLLLGLIAMLVVLETFCELHELKKFRKMFYVKKDKD 156
                                                                                                        A----LQKDQALQTQPQYVAFSFVYILTG----LTVIGAFLNLVVL---RFMTMNAEDEK 255
                                                                                                                                             GFSKQVVAIVHAVLLGFVTVSCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYV 101
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Pred. No. 6e-05;
7; Mismatches 48;
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Pred No. 8.
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Search completed: August 28, 2001, 17:11:45 Job time: 389 sec

HIS PACE BLAMF (USPID)

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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1 MAAPDLLDPKSAAO
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Gapop 10.0 , Gapext 0.5
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    /cgn2_6/ptcdata/2/paa/USO6_COMB.pep:*
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    9 US-09-503-089A-4
US-09-828-746-6
PCT-US9-03826-83
7 US-09-336-643-83
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22 US-09-828-746-2
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Sequence 4, Appli
Sequence 6, Appli
Sequence 83, Appl
Sequence 83, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 45, Appl
Sequence 45, Appl
Sequence 45, Appl
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US-09-655-272-4 US-09-144-914-6 US-09-144-914-6 US-09-144-914-6 US-09-144-914-6 US-09-144-914-6 US-09-144-914-6 US-09-144-914-6 US-09-143-255-P US-00-852-365-7 US-00-852-365-7 US-00-20-543-3-2 US-00-20-445-16-2 US-00-21-38-15-2 US-00-23-470-2 US-00-258-275-4 US-00-258-275-2 US-00-258-275-4 US-00-258-275-4 US-00-258-275-4 US-00-258-275-2 US-00-258-275-4 US-00-258-275-2 US-00-258-275-4 US-00-258-275-2 US-00-278-169-2 US-00-278-1	Query Match Best Local Similarity 100.0%; Matches 411; Conservative 0 Qy 1 MAAPDLLDPKSAAQNSKPRLSFSS	RESULT 1 US-09-503-089A-4 Sequence 4, Application US/09503 GENERAL INFORMATION: APPLICANT: PATEL, AMANDA J. APPLICANT: LESAGE, FLORIAN APPLICANT: LESAGE, FLORIAN APPLICANT: LESAGE, FLORIAN APPLICANT: LAZDUSKI, MICHEL TITLE OF INVENTION: A method f. FILE REFERENCE: f17bl2prov3-hu CURRENT APPLICATION NUMBER: US/ CURRENT FILING DATE: 2000-02-1 NUMBER OF SEQ ID NOS: 5 SOFTWARE: MICTOSOft Word 2000 SEQ ID NO 4 LENGTH: 411 TYPE: PRT ORGANISM: Mus musculus US-09-503-089A-4	420 20.1 499 21	420 20.1 499 21 420 20.1 499 21 420 20.1 499 21 420 20.1 499 21	420 20.1 499 18 420 20.1 499 19 420 20.1 499 19 420 20.1 499 21 420 20.1 499 21	510 24.4 295 23 506 24.2 110 23 420 20.1 499 16 420 20.1 499 17	770.5 36.9 398 20 753.5 36.1 1779 23 753.5 36.1 1785 23 752 36.0 1616 23 640.5 36.6 1068 23 640.5 36.6 1068 23	797 38.1 392 1 797 38.1 392 21 797 38.1 393 18 797 38.1 393 18 797 38.1 419 22 797 38.1 410 23 797 38.1 1314 21 797 38.1 1314 21	11 1864 89.2 370 20 11 1855 88.8 370 15 11 1855 88.8 370 15 11 11 1251.5 59.9 543 1 P1 1251.5 59.9 543 22 11 1250 58.6 724 23 1 18 1207.5 57.8 484 23 1
0 0 0 ° ° ° ° ° ° ° ° ° ° ° ° ° ° ° ° °	COTE 2090; DB 03; Length 411; red. no. 5.1e- 4; mismatches 0; Gap mismatches 0; Gap TVLASRVESDSAIN. NATUSTIFLVVVLYLII 6 TVLASRVESDSAIN. NATUSTIFLVVVLYLII 6 TVLASRVESDSAIN. NATUSTIFLVVVLYLII 6 TVLASRVESDSAIN. NATUSTIFLVVVLYLII 6 TVLASRVESDSAIN. NATUSTIFLVVLYLII 6 TVLAGHACVNSTELDELIOQIVAAINAGIIPLGNS 1	9A Mnaunt the identification of anes nTREK /503,089A	LIGNMENTS sequence	09-735-169A- Sequence 09-735-171-2 Sequence 09-735-171-4 Sequence	09-436-265-201 Sequence 09-561-763-2 Sequence 09-578-169-2 Sequence 00-735-169-2 Sequence	50-223-269-8 Sequence 50-171-487-55-3 Sequence 50-151-2 Sequence 50-259-951-4 X 50-259-951-4 X 50-259-951-4 X 50-259-951-4 X 50-259-951-4 X	99-655-272-2 Sequence 60-212-358-1 Sequence 50-207-416-9 Sequence 50-229-525-3 Sequence 50-212-358-1 Sequence 99-828-746 Sequence	JS00-34983B-55 Sequence J9-729-739-5 Sequence 99-432-470-4 Sequence J9-828-035-2 Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence	99-655-272-4 99-144-914-6 99-144-914-6 99-436-265-P Sequence 1501-14965-7 Sequence 150-207-583-3 Sequence 50-230-445-16-7 Sequence 50-230-445-16-7 Sequence

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US-09-828-746-6
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Best Local Similarity 99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6
LENGTH: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: HOMO SAPIENS
-09-828-746-6
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PRIOR ETLING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: EP 98300570.3
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: UK 9822135.1
PRIOR FILING DATE: 1998-10-09
RUMBER OF SEO ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Conrad Gerald Chapman TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GP-30031-D1
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CURRENT FILING DATE: 2001-04-09
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                                                                                                                             LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD 240
                                                                                                                                                                                                                                          GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS
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AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
                                                                                                            LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD
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RESULT 4 US-09-336-643-83

Sequence 83, Application US/09336643 GENERAL INFORMATION:
APPLICANT: Miller, Andrew

APPLICANT:
APPLICANT:

Curran, Mark Ping Hu

APPLICANT:

Rutter

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APPLICANT: Miller, Andrew
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                                                                                                                                                                                                                                                                                                                                                                                 Matches
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EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER FILING DATE: 1999-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CUTTAN, MARK
TITLE OF INVENTION: NOVEL Human Potassium Chan
EILE REFERENCE: SEQ-15PCT
CURRENT APPLICATION UNMBER: PCT/US99/03826A
CURRENT FILING DATE: 1999-02-22
EARLIER APPLICATION NUMBER: 60/076,687
EARLIER FILING DATE: 1998-02-25
EARLIER FILING DATE: 1998-02-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                  ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHC/ PDIAVIENMK 411
                                                                                                                                                                     SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFC1:\ALLGIPLFGFLLAGVGDQ 180
KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDK SOMATSVKRKLSAELAGNHNQ
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Pred. No. 2.6e-197;
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US-09-336-643-83
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CURRENT FILING DATE: 1999-06-18
EARLIER APPLICATION NUMBER: 60/095,836
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: PCT/US99/03826
EARLIER FILING DATE: 1999-02-22
                                                                                                                                                                                                                                                                                         Sequence 83, Application US/09336643A GENERAL INFORMATION:
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Best Local S
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                                               CURRENT APPLICATION NUMBER: US/09/336,643A CURRENT FILING DATE: 1999-06-18 EARLIER APPLICATION NUMBER: 60/076,687 EARLIER FILING DATE: 1998-08-07 EARLIER APPLICATION NUMBER: 60/116,448 EARLIER FILING DATE: 1999-01-19
                                                                                                                                                                APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium
FILE REFERENCE: SEQ-15P
EARLIER APPLICATION NUMBER: PCT/US99/03826 EARLIER FILING DATE: 1999-02-22 NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                    APPLICANT: Hu, Ping
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TYPE: PRT
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TITLE OF INVENTION: Novel
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Pred. No. 2.6e-199;
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                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09828746 GENERAL INFORMATION:
                                                                         Query Match
Best Local Similarity
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                                                             Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: GP-30031-D1
CURRENT APPLICATION NUMBER: US/09/828,746
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Conrad Gerald Chapman TITLE OF INVENTION: NOVEL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Helen Jane Meadows APPLICANT: Conrad Gerald Chap
                                                                                                                                                               LENGTH: 41
TYPE: PRT
                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/236,080 PRIOR FILING DATE: 1999-01-25
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                                                           Score 2044; DB ::
Pred. No. 2.6e-1:
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Pred. No. 2
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APPLICANT: HONORE, ERIC
APPLICANT: LESGGE, FLORIAN
APPLICANT: LAZDUSKI, MICHEL
TITLE OF INVENTION: A method for the identification of anesthetics
FILE REFERENCE: f17b12prov3-humanTREK
CURRENT APPLICATION NUMBER: US/09/503,089A
CURRENT FILING DATE: 200-02-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Word 2000
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Applicat GENERAL INFORMATION:
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US-08-816-011-45
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FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
ATTORNEY_AGENT INFORMATION:
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32,46
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2134
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Pausch, Mark H.

TITLE OF INVENTION: Potassium Channels, Nu: Gotide Sequences
TITLE OF INVENTION: Encoding Them, and Meth dis of Using Same
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #10, Version #1.20
CURRENT APPLICATION DATA:
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mer.meAX: 201-683-4117
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STATE: New Jersey
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 426 amino acids
                                                                                                                SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCII:ALLGIPLFGFLLAGVGDQ 180
                                                                                     LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCV:.. VALPAVIFKHIEGWSALD 240
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; Sequence 45, Application US/08816011A
; GENERAL INFORMATION:
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Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acid
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ATTORNEY/AGENT INFORMATION:
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CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
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REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32
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TOPOLOGY: li
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FILING DATE: 11-MAR-1997
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                                                                   LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALD
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AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
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                                                                                                              SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 195
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Encoding Them,
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95.1%; Pred, No. 6.3e-196;
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US-08-816-011C-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 45
LENGTH: 426
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                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 391; Conserv
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TITLE OF INVENTION: AND METHODS OF USING S,
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011C
CURRENT FILING DATE: 1997-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/332,312 PRIOR FILING DATE: 1994-10-31
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APPLICANT: Price, Laura &
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                                                                KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDA 👸 ATSVKRKLSAELAGNHNO
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AIYEVVITLTTIGEGDYVAGGSDIEYLDEYKPVVWEWIT: LAYEAAVLSMIGDWLRVIS
AIYEVVITLTTIGEGDYVAGGSDIEYLDEYKPVVWEWIT: LAYEAAVLSMIGDWLRVIS
AIYEVVITLTTIGEGDYVAGGSDIEYLDEYKPVVWEWIT: LAYEAAVLSMIGDWLRVIS
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US-09-655-272-4
; Sequence 4, Application
; GENERAL INFORMATION:
; APPLICANT: HONORE, ERIC
; APPLICANT: FINK, MICHE

ERIC

us/09655272

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APPLICANT: LAZDUNSKI, MICHEL
APPLICANT: LESAGE, FLORIAN
APPLICANT: LESAGE, FLORIAN
APPLICANT: DUPRAT, FABRICE
TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS
TITLE OF INVENTION: ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AND THE USE
TITLE OF INVENTION: OF SAID CHANNELS IN DRUG SCREENING
FILE REFERENCE: 1383-00
CURRENT FAPLICATION NUMBER: US/09/655,272
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: PCT/FR99/00404
PRIOR APPLICATION NUMBER: FCT/FR99/00404
PRIOR APPLICATION NUMBER: FCT/FR99/00404
PRIOR FILING DATE: 1998-02-23
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 5
                                                          Sequence 8, Application US/09144914
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
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US-09-144-914-8
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LENGTH: 370
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Best Local Similarity
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OTHER INFORMATION: Description
-09-655-272-4
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                EARLIER
                              EARLIER APPLICATION NUMBER: 08/749,816 EARLIER FILING DATE: 1996-11-15
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                                                                                                                                                                                TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN TITLE OF INVENTION: CLONING AND THEIR USE, TITLE OF INVENTION: DRUGS FILE REFERENCE: 1201-CLT2-00 CURRENT APPLICATION NUMBER: US/09/436,265 CURRENT FILING DATE: 1999-11-08 PRIOR APPLICATION NUMBER: 60/095,234 PRIOR FILING DATE: 1998-08-04 PRIOR FILING DATE: 1998-08-04 PRIOR FILING DATE: 1998-08-04 PRIOR APPLICATION NUMBER: 60/107,692 PRIOR FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 32 SOFTWARE: PATENTIN PRIOR FILING DATE: 1996-11-09 NUMBER OF SEQ ID NOS: 32 SOFTWARE: PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENTIN PATENT
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APPLICANT: DUPRAT, FABRICE
APPLICANT: LESAGE, FLORIAN
APPLICANT: FINK, MICHEL
APPLICANT: SALINAS, MIGUEL
APPLICANT: FARMAN, NICOLETTE
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EARLIER APPLICATION NUMBER: FR 96/01565
EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
LENGTH: 370
TYPE: PRT
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Best Local Similarity
Matches 366; Conserv
                                                                                                                                         SEQ ID NO 8
LENGTH: 370
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PCT-US01-14965-73; Sequence 73, Applica; GENERAL INFORMATION:
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; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn version
; SEQ ID NO 73
; LENGTH: 543
; TYPE: PRT
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                                                                                                                                                                                                              CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/206,526
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
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Best Local
                                                                  PRIOR APPLICATION NUMBER: 60/223, 245
PRIOR FILING DATE: 2000-08-04
NUMBER OF SPORTS
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ruble, Cara L.
TITLE OF INVENTION: Human Ion Channels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Pharmacia & Upjohn Company APPLICANT: Roberds, Steven L.
                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: PCT/US01/14965
CURRENT FILING DATE: 2001-05-10
                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 00133.PCT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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nes 366; Conserv
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                                                                                                                 APPLICATION NUMBER: 60/237,873 FILING DATE: 2000-10-04
                                                                                                                                                   APPLICATION NUMBER: 60/216,893 FILING DATE: 2000-07-17
                                                                                                                                                                                 APPLICATION NUMBER: 60/207,093 FILING DATE: 2000-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ
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Benjamin, Christopher
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Pred. No. 4.4e-180;
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PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/2016,893
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/237,873
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 60/233,245
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 60/233,245
PRIOR FILING DATE: 2000-08-04
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ORGANISM: Homo sapiens
US-09-852-386-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens PCT-US01-14965-73
                                                                    SOFTWARE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 73, Application US/09852386 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 59.9
Best Local Similarity 64.3
Matches 247; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/852,386
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Karnovsky, Alla M. APPLICANT: Ruble, Cara L. TITLE OF INVENTION: Human Ion Channels FILE REFERENCE: 00133.US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Roberds, Steven L. APPLICANT: Benjamin, Christopher
                                                                                                 NUMBER OF SEQ ID NOS: 88
                                 LENGTH: 54
TYPE: PRT
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                                                                                    PatentIn
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Search completed: August 28, 2001, 17:11:14 Job time: $603\ sec$

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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2100
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/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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     DB
       US-09-336-643-83

US-09-431-367B-2

US-09-431-367B-5

US-09-746-491-60

US-09-746-491-59

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US-09-378-614-2

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; TYPE: PRT
; ORGANISM: Homo sapiens
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                                                                                                              Sequence 5, Application US/09431367B
GENERAL INFORMATION:
APPLICANT: CURTIS, ROTY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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Best Local Similarity
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TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
                  PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
                                                                           CURRENT APPLICATION NUMBER: US/09/431,367B CURRENT FILING DATE: 1999-11-01
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SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                            268 E-SSPHS-----RKALQVKGSTASKDVNIFSFLSKKEETY 301
                                                                                                                                                                                                                                                                                                                                  353 ELAGNHNQELTPCRRTLSVNHLTNERDV--LPPLLKTESIY
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; TYPE: PRT
; ORGANISM: Homo
US-09-431-367B-5
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SOFTWARE: PatentIn Ver. 2:
SEQ ID NO 15
LENGTH: 394
TYPE: PRT
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Best Local :
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APPLICANT: Powers, Scott
APPLICANT: Tularik Inc.
TITLE OF INVENTION: KCNB: A Novel Potassium
FILE REFERENCE: 018781-004010US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-03-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/186,951
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                          ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAX; TTIGFGNISPRTEGGKI 157
ISTIIFILFGCVLFVALPAIIFKHIEGWSALDAIYFVV. : CTTIGFGDYVAGGSD--IEY
                                      FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKG! 'MRRAD-----VSM 156
                                                                        FCIIYALLGIPLFGFLLAGVGDQLGTIF-----GKGAKVEDTFIKWNVSQTKIRI 208
                                                                                                                ELERVVLRL-KPHKAGV-----QWRFAGSFYF7
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                                                                                                                                                                                       MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERCE, CERQQELRARYNLSQGGYE
                                                                                                                                                                                                                                                                     91;
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31.0%;
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Pred. No. 1.56'.'
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APPLICANT: Mu, David

APPLICANT: Powers, Scott

APPLICANT: Tularik Inc.

TITLE OF INVENTION: KCNB: A Novel Potassium Ch.

FILE REFERENCE: 018781-004010US

CURRENT APPLICATION NUMBER: US/09/798,584

CURRENT FILING DATE: 2001-03-03

PRIOR APPLICATION NUMBER: US 60/186,951

PRIOR APPLICATION NUMBER: 05 60/186,951

PRIOR FILING DATE: 2000-03-03
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US-09-798-584-1
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PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 60
LENGTH: 365
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic
FILE REFERENCE: 15966-621
                                                                                                                                                                                                            Sequence 1, Application US/09798584 GENERAL INFORMATION:
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Best Local
NUMBER OF SEQ ID NOS: 18 SOFTWARE: PatentIn Ver. 3 SEQ ID NO 1
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CURRENT FILING DATE: 2000-12-20
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SEQ ID NO 8
LENGTH: 313
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Best Local Similarity
Matches 83; Conserv
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Best Local Similarity
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PRIOR FILING DATE: 1999-03-01
NUMBER OF SEQ ID NOS: 12
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; OTHER INFORMATION: human KCNB (Potassium Chan.e. US-09-798-584-1
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GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MC
FILE REFERENCE: MNI-074CP
CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
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                                                                                  57 YLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCV
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                 LGNTSNQIS----HWDLGSSFFFAGTVITTIGFGNISPF #:GGKLFCIIYALLGIPLFGF 172
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LANASGSANASDPAWDFASALFFASTLITTVGYGYTTPL.:DAGKAFSIAFALLGVPTTML 136
                                                                             YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCV
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                                                                                                                                                           16.6%; Score 348; DB 34.4%; Pred. No. 2.6e tive 42; Mismatches
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27.0%; Pred. No. 2.4 4,1
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PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR APPLICATION NUMBER: PCT/US99/03826
PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81
                                                                                     RESULT 9
US-09-746-491-59
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Sequence 59, Application US/09746491
GENERAL INFORMATION:
APPLICANT: BUTGESS, Catherine E.
TITLE OF INVENTION: Novel Proteins and
FILE REFERENCE: 15966-621
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/336,643
CURRENT FILING DATE: 1999-06-18
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                                                                                                                                                                                                                                   AHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALYKVLVTVYLFLGLVAMVLV
                                                                                                                                                                                                                                                         KHI-EGWSALDAIYFVVITLTTIGFGDYVAGGSDIE-YLDFYKPVVWFWILVGLAYFAAV
                                                                                                                                                                                                                                                                                                                                         LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVA--LPAIIF 230
                                                                                                                                                                                                                                                                                                                                                                             LANASGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTML 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCVAAPALDAFVERVLAAGRLGRVV 76
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                                                                                                                                                                                                                                                                                                         LLTASAQRLSLL----LTHVPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCFLVPAVIF 192
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                    Nucleic Acids
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             Encoding
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CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEO ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 59
LENGTH: 330
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                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mus musculus US-09-746-491-61
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US-09-746-491-61
; Sequence 61, Application US/09746491
; GENERAL INFORMATION:
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SEQ ID NO 61
LENGTH: 258
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: Novel Proteins and Nucleic
FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
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PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
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                                   158
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                  FCIIYALLGIPLEGFULAGVGDQLGTIFGKGIAKVEDTETKUNVSQTK------IRI 208
                                                                     ELERVVLRL-KPHKAGV------QWRFAGSFYFA(TV[TTIGYGHAAPSTDGGKV 108
                                                                                          ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                           MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIEROKLELRQLELRARYNLSEGGYE 60
                                                                                                                                                              MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQR1TIV1QKQTFISQHSCVNS--T 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPLTLVTFQSLGERLNAVVRRLLLAAKCCLGLRWTCVSTE----NLVVAGLLACAATLAL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPLFGFLLAGVGDQLGTIFGKGIAKVEDTF-IKWNVSQTKIHISTIIFILFGCVLFVAL 225
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FCMFYALLGIPLTLVMFQSLGERI-----NTFVRYLLHRAKRGLGMRHAEVSM 156
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hilarity 34.9%;
Conservative 4;
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                                                                                                                                                                                                                 16.3%; Score 342.5; DB 5: 30.0%; Pred. No. 6.3e-24; tive 61; Mismatches 54;
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Pred. No. 3.1e-24;
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US-09-746-491-58
Sequence 58, Application US/09746491
GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic Acids; FILE REFERENCE: 15966-621
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                                SEQ ID NO 22
LENGTH: 393
TYPE: PRT
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CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 58
LENGTH: 330
                                                                                                                                                                                                                                                                Sequence 22, Application US/09746491 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                      CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Novel Proteins and Nucleic Acids
FILE REFERENCE: 15966-621
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ORGANISM: Homo sapiens
FEATURE:
            ORGANISM: Homo sapiens
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Pred. No. 1.7e-23;
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NAME/KEY: VARIANT
LOCATION: (340)
OTHER INFORMATION: Wherein Xaa is any amino action
OTHER INFORMATION: specification
US-09-746-491-22
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-367B-11
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
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Matches
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Best Local Similarity 20.8%;
Matches 77; Conservative
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CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
                                   210
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                                   KPADEAVPQIIISAEELPGPKLGTCPSRPSCSMELFERSHALEKQNTLQLPPQAMERSNS 269
                                                                                                         CMLYALEGIPLMFLVLTDTGDILATILSTSYNRERKEPF: FRPLLSKWCPKSLFKKKPDP
                                                                                                                                                                            ETVVEDRKQDLQGHLQKVKPQWFNRTTHWSFLSSLFFCc: (1:STVGYGYIYPVTRLGKYL 149
                                                                                                                                                                                                                                                LVTYALVGAVVFSAIE------DGQVLVA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPLFGFLLAGVGDQLGTIFGKGIAKVEDTF-IKWNVSQ1KIRIISTIIFILFGCVLFVAL 225
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                                                                                                                                                                                              ----NQISHWDLGSSEEFA: TTI
                                                                                                                                                                                                                                                                                                                        38;
                                                                                                                                                                                                                                                                                                      Score 205; DB 5; Long.
Pred. No. 4.6e-11;
Wismatches 83; Indels 172;
-KIRIISTIIF1LFGCVLFVALPAIIFKHIEG
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US-09-336-643-16
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                                                                                                     Sequence 1386, Application US/09760469
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 16 LENGTH: 197
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1983
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/076,687
PRIOR TILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US99/03826 PRIOR FILING DATE: 1999-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
FILE REFERENCE: SEQ-15P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Miller, Andrew P. APPLICANT: Curran, Mark Edw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hu, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                318 -- TANVTAE 324
                                                                                                                                                                                                                                                                                                                                                                                                         266 YLDFYKPVVWF-----WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEW 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 IISTIIFILFGCVLFVALPAIIFKHIEG-WSALDAIYFVVITLTTIGFGDYVAG-GSDIE 265
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                                                                                                                                                                                                                                                                                                                                                                   -----PVIYHLGQLALLGYLLLGL-----LAML-----LAVETFSELPQVRAMGKFF 159
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; SEQ ID NO 1386
LENGTH: 205
; TYPE: PRT
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                                                                                                                                       197 IKWNVSQTKIRIISTII--FILFGCVLFVALPAIIFKH: GWSALDAIYFVVITLTTIG 253
                             308 GEFRAHAAE 316
156 DEDQVHIIE 164
                                                                                         254 FGDYVAG-GSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISK-----KTKEEV 307
                                                              97
                                                                                                                   39 IRWGFSKQVVAIVHAVLLGFVTVSCFFFI--PAAVESVY NELESEVFCFISLSTIG 96
                                                           LGDYVPGEGYNQKFRELYKIGITCYLLLGLIAMLVVLETECE-LHELKKFRKMFYVKKDK 155
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30.2%;
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Search completed: August 28, 2001, 17:11:44 Job time: 388 sec

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Result No.

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Sequence 8, A	Sequence 2, Appl	Sequence 21, App	Sequence 9, Appl	Sequence 12101	Sequence 12102	Sequence 1266,	Sequence 6145, Ap	Sequence 612,	Sequence 4777,	Sequence 4620,	Sequence 12322	Sequence 13186, A	Sequence 1905,	Sequence 8812,	Sequence 7029,	Sequence 6, Appl.	sequence 23, Appl

ALIGNMENTS

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RESULT 1

US-09-336-643-83

US-09-336-643-83

Sequence 83, Application US/09336643

EAPPLICANT: Miller, Andrew P.

APPLICANT: MILLER, Mark Edward

APPLICANT: Hu, Ping

APPLICANT: Wang, Jian-Walluman Potassium Che

TITLE OF INVENTION: Novel Human Potassium Che

FILE REFERENCE: SEQ-15P

CURRENT FILLING DATE: 1999-06-18

PRIOR APPLICATION NUMBER: 60/076,687

PRIOR FILLING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: 60/16,448

PRIOR APPLICATION NUMBER: 60/176,687

PRIOR FILLING DATE: 1999-01-19

PRIOR APPLICATION NUMBER: PCT/US99/03826

PRIOR FILLING DATE: 1999-02-22

NUMBER OF SEQ ID NOS: 87

SOFTWARE: FastSEQ for Windows Version 4.0

1 SEQ ID NO 83

LENGTH: All
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; TYPE: PRT
; ORGANISM: H.
US-09-336-643-83
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Best Local Sin
Matches 396;
             241
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GENERAL INFORMATION:
APPLICANT: CUITIS, RORY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL
FILE REFERENCE: MNI-074CP
                                                                                                                                                                                     Sequence 5, Application US/09431367B GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
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CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
                                    CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
                                                                                                                         APPLICANT: Curtis, Rory A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES
FILE REFERENCE: MNI-074CP
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SOFTWARE: PatentIn Ver.
                     NUMBER OF SEQ ID NOS: 12
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                                                                                                                                                                                                                                                                                                                  268 E-SSPHS-----RKALQVKGSTASKDVNIFSFLSKKEETY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGLAW----LSLF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHI 233
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; SEQ ID NO 5;
LENGTH: 332;
TYPE: PRT;
ORGANISM: Homo sapiens
US-09-431-367B-5
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                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 394
TYPE: PRT
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Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: Powers, Scott
APPLICANT: Powers, Scott
APPLICANT: TULATIK Inc.
TITLE OF INVENTION: KCNB: A Novel Potass.
FILE REFERENCE: 018781-004010US
CURRENT APPLICATION NUMBER: US/09/798,584
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170 FGFLLAGVGDQLGTIFGKGI----AKVEDTFIKWNVSQTKIF: ISTIIFILFGCVLFVAL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
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                                                                                                   61
                                                                                                                                                                                        42 MKWKTVSTIFLVV--VLYLIIGAAVFKALEQPQEISQR., AVIOKOTFIACHACVNS--T 97
                                                                                                                                                                                                                                                          Local Similarity
                              PPLLFSHMEGWSYTEGFYFAFITLSTVGFGDYVIGMNPSQRYPLWYKNNVSLWILFGMAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLAYLAYLALGTGVFWTLEGRAAQDSSRSFQRDKWELL()...: LDRPALDSLIRDVVQA 84
                                                                                                                                                                      MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERCH..ELRQQELRARYNLSQGGYE
ISTIIFILFGCVLFVALPAVIFKHIEGWSALDAIYFVVITL?T1GFGDYVAGGSD--IEY
                                                                                                                                                                                                                                          109;
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                                                                                                                                                                                                                                                      17.7%; Score 370; DB : Length 394; 28.0%; Pred. No. 1.4e-75;
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Pred. No. 2.9e-2r
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49;

Gaps

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99

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CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEO ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 59
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-09-746-491-59
                                                                                        RESULT 6
US-09-746-491-60
US-09-746-491-60
; Sequence 60, Application US/09746491
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Novel Proteins and Nucleic
; FILE REFERENCE: 159-66-621
; FILE REFERENCE: 159-66-621
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GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding
FILE REFERENCE: 15966-621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                   CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                           175 AVAFSHFEGWTFFHAYYYCFITLTTIGFGDFVALQSG-EALQRKLPYVAFSFLYILLGLT 233
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                                                                                                                                                                                                                                                                                                                                                                                                             AVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF----WILVGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLFGFLLAGVGDQLGTIFGKGIAKVEDTF-IKWNVSQTKIRIISTIIFILFGCVLFVALP 226
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                                                                                                                         Acids
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US-09-746-491-60
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SEQ ID NO 60
LENGTH: 365
TYPE: PRT
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LENGTH: 258
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Best Local Similarity
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Matches 94; Conserv
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CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Burgess, Catherine E. TITLE OF INVENTION: Novel Proteins and Nucleic Acids FILE REFERENCE: 15966-621
                       107
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                                                            156 KIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDIFIKWNVSQTK------I 206
                                                                                                                                          100 D-ELIQQIVAAI---NAGIIPLGNSSNQVSHWDLGSSFFFRAC.VITTIGFGNISPRTEGG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 HISEEARQVRQR 285
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                                                                                                     58 GYEELERVVLRLKPHKAGV
                                                                                                                                                                                                                          42 MKWKTVSTIFLVV--VLYLIIGAAVFKALEQPQEISQRTTIV QKQTFIAQHACVNSTEL 99
                                                                                                                                                                                   1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERORLFORQLEURARY---NLSEG
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                       KVFCMFYALLGIPLTLVMFQSLGERI-----
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GENERAL INFORMATION:
APPLICANT: Burgess, Catherine E.
TITLE OF INVENTION: Novel Proteins and Nucleic
FILE REFERENCE: 1966-621
                                                                                                    NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/09746491 GENERAL INFORMATION:
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 58
LENGTH: 330
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                                                                                                                                                                             PRIOR FILING DATE: 1999-12-21
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: USSN 60/171,329
                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 2000-12-20
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CURRENT FILING DATE: 2000-12-20
                                                                TYPE: PRT
NAME/KEY: VARIANT
                                      ORGANISM: Homo sapiens
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                      FEATURE
                                                                                      LENGTH: 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVIEKHIEGWSALDAIYFVVITLTTIGEGDYVAGGSDIEYLDFYKPVVWF---WILVGLA 283
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APPLICANY: Powers, Scott
APPLICANY: Tularik Inc.
TITLE OF INVENTION: KCNB: A Novel Potassium
FILE REFERENCE: 018781-004010US
CURRENT FILING DATE: 2001-03-03
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR APPLICATION NUMBER: US 60/186,951
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: human KCNB (Potassium Channel expressed in US-09-798-584-1
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                                                                                                                                                                                                                                                                                                                              Matches 104;
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Mu, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (340)
109
                                                                                                                                                                                          100 DELIQQIVAA--INAGIIPLGNSSNQVSHWDLGSSFFFAGIVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 VIGAFLNLVVLRFLVASADW 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 YFAAVLSMI ------GDW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 PLFGFLLAGVGDQLGTIFGKGIAKVEDTF-IKWNVSQTK!RIISTIIFILFGCVLFVALP 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 -- INAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGN. RTEGGKIFCIIYALLGI 167
                                                                                                                                                      60
                                                                                                                                                                                                                                                                42 MKWKTVSTIFLVV--VLYLIIGAAVFKALEQPQEISQRI? VIQKQTFIAQHACVNSTEL 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 IFLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFTAQHACVNSTELDELIQQIVAA 109
                                                                                                                                                                                                                                          1 MKRONVRTLSLIVCTFTYLLVGAAVFDALESDHEMREEEK! KAEEIRIKGKYN-ISSEDY 59
                                                                                                                                                    RQLELVILQSEPHRAGV------QWKFAGSFYF7: "VITTIGYGHAAPGTDAGKA 108
                                                                  FCMFYAVLGIPLTLVMFQSLGERM------NTFVRY LKRIKKCCGMRNTDVSM 156
                                                                                                        FCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKW-----NVSQTKIRI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVAFSHFEGWTFFHAYYYCFITLTTIGFGDFVALQSG-EALQRKLPYVAFSFLYILLGLT 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF:--WILVGLA 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLTLVTFQSLGERLNAVVRRLLLAAKCCLGLRWTCVSTE - - - - NLVVAGLLACAATLALG
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                                                                                                                                                                                                                                                                                                                                                16.4%; Score 342.5; DB 5; 26.5%; Pred. No. 4.7e-21;
                                                                                                                                                                                                                                                                                                                            78;
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GENERAL INFORMATION:
APPLICANT: CURTLIS, RORY A.J.
TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES
FILE REFERENCE: MNI-074CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 313
                                                                                                                                                                                 Sequence 81, Application US/09336643 GENERAL INFORMATION:
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-09-431-367B-8
                                    APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
FILE REFERENCE: SEO-15P
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PRIOR APPLICATION NUMBER: 09/259,951
PRIOR FILING DATE: 1999-03-01
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  CURRENT APPLICATION NUMBER: US/09/336,643
CURRENT FILING DATE: 1999-06-18
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                                                                                                                                                                                                                                                                                                          253 L
                                                                                                                                                                                                                                                                                                                                                                                                                    231 KHI-EGWSALDAIYFVVITLTTIGFGDYVAGGSDIE-YLDFYKPVVWFWILVGLAYFAAV 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVA--LPAVIF 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 VTAEFKETRRRLSVEI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGNSSNQVS----HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLTASAQRLSLL----LTHVPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCFLVPAVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LANASGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTML 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCVAAPALDAFVERVLAAGRLGRVV 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.4%; Score 342; DB 5; Length 313; 34.4%; Pred. No. 4e-24;
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; LENGTH: 313
; TYPE: PRT
; ORGANISM: H.
US-09-336-643-81
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; Sequence 11, Application US/0
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT ; ORGANISM: Homo sapiens: US-09-431-367B-11
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Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/259,951 PRIOR FILING DATE: 1999-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/431,367B
CURRENT FILING DATE: 1999-11-01
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PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL FILE REFERENCE: MNI-074CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 87
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 401
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159 CIIYALLGIPLEGELLAGVGDQLGTI-----FGKG1: Chreikw----
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                                                                                                                                                                                                                                          Match 10.1%; Score 212; DB Local Similarity 20.8%; Pred. No. 6.7e-
                                           90 ETVVEDRKQDLQGHLQKVKPQWFNRTTHWSFLSSLFFCCT.
                                                                                                                                   54 VVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHA: ::TELDELIQQIVAAINAG 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09431367B
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                                                                                       ----NQVSHWDLGSSFFFAG
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                                         STVGYGYIYPVTRLGKYL 149
                                                                                                                                   DGEFEKFLEELCRILNCS
                                                                                       : FIGFGNISPRTEGGKIF 158
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                                                                                                                                                                                                                                                                 Length 401;
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US-09-760-469-1386
Sequence 1386, Application US/09760469
GENERAL INFORMATION:
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US-09-336-643-16
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CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076,687
PRIOR FILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR FILING DATE: 1999-01-19
PRIOR PRIOR FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/09336643
GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
APPLICANT: Curran, Mark Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.3%; Score 152.5; DB 5; Best Local Similarity 27.5%; Pred. No. 8.1e-07; Matches 52; Conservative 39; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
FILE REFERENCE: SEQ-15P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                       160 RPSGPVTAE 168
                                                                                                                                                                                 318 -- TANVTAE 324
                                                                                                                                                                                                                                                                                                                                                         208 IISTIIFILFGCVLFVALPAVIFKHIEG-WSALDAIYFVVITLTTIGFGDYVAG-GSDIE 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 ISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIR 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 CPELVLGRLSYSIISNLDEVGQQVERLDIPLPIIALIVFAYISCAAAI-LPF----- 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          266 YLDFYKPVVWF-----WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEW 317
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                                                                                                                                                                                                                                                                                                                    58 LLQAVALGLLVASSFVLLPALVLWGLQGDCSLLGAVYFCFSSLSTIGLEDLLPGRGRSLH 117
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                                                                                                                                                                                                                           -----PVIYHLGQLALLGYLLLGL-----LAML-----LAVETFSELPQVRAMGKFF 159
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                                                                                                                                                                                                                                                                                                                                                                                                        MAPLSPGGKAFCMVYAALGLPASLALVATLRHCLLPVLSRPRAWVA----VHWQLSPARAA 57
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Rutter, Marc
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Search completed: August 28, 2001, 17:11:45 Job time: 389 sec

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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1386
LENGTH: 205
TYPE: PRT
ORGANISM: Homo sapiens
US-09-760-469-1386
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Best Local Similarity
Matches 39; Conserv
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFEROCE: P7254
CURRENT APPLICATION NUMBER: US/09/760,469
CURRENT FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prior application data removed - consult PALM of file wrapper NUMBER OF SEQ ID NOS: 1983
                                                                                                                                                                                                    197 IKWNVSQTKIRIISTII--FILFGCVLFVALPAVIFKH
156 DEDQVHIIE 164
                                      308 GEFRAHAAE 316
                                                                                                                   254 FGDYVAG-GSDIEYLDFYKPVVWFWILVGLAYFAAVLSKIGDWLRVISK-----KTKEEV 307
                                                                          97 LGDYVPGEGYNQKFRELYKIGITCYLLLGLIAMLVVLET CE-LHELKKFRKMFYVKKDK 155
                                                                                                                                                           39 IRWGFSKQVVAIVHAVLLGFVTVSCFFFI--PAAVFSVL DDWNFLESFYFCFISLSTIG 96
                                                                                                                                                                                                                                               Conservative
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Perfect score:
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Maximum DB seq length: 200000000
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Gapop 10.0 , Gapext 0.5
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2100
1 MAAPDLLDPKSAAQNSKPRL.....LNGLTPHCAGEEIAVIENIK 411
: //cgn2_6/ptodata/2/paa/US08_COMB.pep: *
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:/cgn2_6/ptodata/2/paa/US07_COMB.pep: *
:/cgn2_6/ptodata/2/paa/US080_COMB.pep: *
:/cgn2_6/ptodata/2/paa/US081_COMB.pep: *
:/cgn2_6/ptodata/2/paa/US082_COMB.pep: *
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Copyright (c) 1993 - 2000 Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2035	2041	2062	2062	2062	2095	2095	2095	2095	2100	Score	
96.9	97.2	98.2	98.2	98.2	99.8	99.8	99.8	99.8	100.0	Match Length DB	Ouerv
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Sequence 6, Appli	Sequence 4, Appli	Sequence 45, Appl	Sequence 45, Appl	Sequence 45, Appl	Sequence 2, Appli	Sequence 83, Appl	Sequence 83, Appl	Sequence 83, Appl	Sequence 2, Appli	Description	

4	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
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US-09-735-171A	9-735-17	-09-735-17	US-09-735-169A	-09-735-16	5-169	-09-561-76	-09-436-	-09-357-425-6	-951-	9-259-951-	0-223-26	- 1	US-09-828-746-4	US-60-212-358-1:5	-60-229-	-60-2	US-60-212-358-1 '	-09-655-27	-09-729-73	-US00-349	-60-258-275-4	-09-828-035-	432-470-4	-09-432-470-	-09-729-739-	T-US00-34983	230-445-	-60-216-547-	-207-58	-852-386-7	65-	-09-436-265-	-09-144-9	US-09-655-272-4
2,	e 4,	2	e 2,	e 4,	e 2,	2,	28,	, 0	4,	2	8,	594		19	331,		133,	N	e 29,	29, p	424, Ap	'n	4,	N	e 55,	55, ,	1632	10, App	376,	e 73,	73,	8, Appl	8, App	Sequence 4, Appli

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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 83
LENGTH: 411
TYPE: PRT
ORGANISM: H. sapiens
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 410; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/076,687
EARLIER FILING DATE: 1998-02-25
EARLIER FOLICATION NUMBER: 60/095,836
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER FILING DATE: 1999-01-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: PCT/US99/03826A CURRENT FILING DATE: 1999-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Novel Human Potassium Channels FILE REFERENCE: SEQ-15PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Miller, Andrew APPLICANT: Curran, Mark
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                               AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
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                                                                                                         LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD 240
                                                                                                                                                                                                                                 GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIPLGNT 120
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                                                                                           LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD
                                                                                                                                                      SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
                                                                                                                                                                    SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGF1LAGVGDQ 180
                                                                                                                                                                                                              GATVFKALEOPHEISORTTIVIOKOTFISOHSCVNSTELDELIQOIVAAINAGIIPLGNT 120
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                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                     99.8%;
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Pred. No. 5.2e
1; Mismatches
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APPLICANT: Miller, Andrew
APPLICANT: Curran, Mark
APPLICANT: Curran, Mark
APPLICANT: Ping Hu
APPLICANT: Marc Rutter
APPLICANT: Marc Rutter
APPLICANT: Marc Rutter
APPLICANT: Marc Rutter
APPLICANTON: Novel Human Potassium Charile Reference: Seo-15p
CURRENT APPLICATION NUMBER: US/09/336,643
CURRENT FILING DATE: 1999-06-18
EARLIER APPLICATION NUMBER: 60/095,836
EARLIER FILING DATE: 1998-08-07
EARLIER FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER APPLICATION NUMBER: PCT/US99/03826
EARLIER APPLICATION NUMBER: PCT/US99/03826
EARLIER FILING DATE: 1999-02-22
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; ORGANISM: H.
US-09-336-643-83
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Best Local :
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SOFTWARE: FastSEQ for Windows Version
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AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVWFWII * AYFAAVLSNIGDWLRVIS
                                                                                                                                                             410;
                                                                     KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDK: CATSIKRKLSAELAGNHNQ
                                                                                                                                                                                                                                                                                                                               MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTIN. KWKTVSTIFLVVVLYLII
                                                       KKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHNQ
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RESULT 4
US-09-336-643-83
Sequence 83, Application US/09336643A
GENERAL INFORMATION:

APPLICANT: Miller, Andrew

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; ORGANISM: H.
US-09-336-643-83
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CURRENT APPLICATION NUMBER: US/09/828,746
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 09/236,080
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: EP 98300570.3
PRIOR APPLICATION NUMBER: EP 98300570.3
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: UK 9822135.1
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 6
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EARLIER APPLICATION NUMBER: 60/076,687
EARLIER FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/116,448
EARLIER FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: PCT/US99/03826
EARLIER FILING DATE: 1999-02-22
NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                                                                           Sequence 2, Application US/09828746 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                    APPLICANT: Helen Jane Meadows
APPLICANT: Conrad Gerald Chapman
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30031-D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Curran, Mark Edward
APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: Novel Human Potassium Channels
FILE REFERENCE: SEQ-15P
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Pred. No. 5.
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; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO 5
US-09-828-746-2
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Best Local S
Matches 410
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GENERAL INFORMATION:
APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
SEQ ID NO 2
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2134
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                            CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale F.
                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
TITLE OF INVENTION: Encoding Them, and Metha is of Using Same
                                                                                                                                                                                                                                                CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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CITY: F
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                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 11-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKF JRATSIKRKLSAELAGNHNQ 360
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410; Conserv
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One Campus Drive
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                                                                                                                             US/08/816,011
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                                                                                                                                                         Version
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                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC COMPATIBLE
OPERATING SYSTEM: PC COMPATIBLE
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,011A
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
ATTORNETY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45, Application US/08816011A GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 426 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Potass
TITLE OF INVENTION: Encodi
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: American
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2134
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                   ZIP:
                                                                                                                                                                                                                                                                                                  CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Potassium Channels, Nucleotide Sequences Encoding Them, and Methods of Using Same
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                                         32,421-C2
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Pred. No. 1.2e-199;
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APPLICANT: Pausch, Mark H
APPLICANT: Price, Laura H
TITLE OF INVENTION: POTASSIIM CHANNELS, NUCLEC TITLE OF INVENTION: AND METHODS OF USING SAMI:
FILE REFERENCE: 01142.0122 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/08/816,011C
CURRENT FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: 08/332,312
PRIOR FILING DATE: 1994-10-31
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR APPLICATION NUMBER: PCT/US95/14364
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                                                                                                                       US-08-816-011C-45
                                                                                                                                                                    SOFTWARE: PatentIn Ver.
SEQ ID NO 45
LENGTH: 426
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                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45, Application US/08816011C
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                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 64
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                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                        TYPE: PRT
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LENGTH: 426 amino acid
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                                Local Similarity
nes 405; Conserv
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TYPE: amino acid
STRANDEDNESS: single
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1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTinVSKWKTVSTIFLVVVLYLII 60
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                                  Conservative
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98.5%;
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                                               Score 2062; Db 12; Pred. No. 1.2e-199:
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-503-089A-4
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US-09-503-089A-4
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Matches
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                                                                                                                                                                                                                                                                                                                    SEQ ID
                                                                                                                                                                                                                                                                                                                                                APPLICANT: LAZDUSKI, MICHEL
TITLE OF INVENTION: A method for the identification
FILE REFERENCE: f17b12prov3-humanTREK
CURRENT APPLICATION NUMBER: US/09/503,089A
CURRENT FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: PATEL, AMANDA J.
APPLICANT: HONORE, ERIC
APPLICANT: LESAGE, FLORIAN
APPLICANT: ROMEY, GEORGES
                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Microsoft Word 2000
                                                                                                                                                                                                                    Local Sim:
hes 395;
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                                                                                                                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                    NO 4
SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
                                                                                                                              LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALD
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                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                             97.2%; Score 2041; DB 19; 96.1%; Pred. No. 1.6e-197;
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                                                                                                                                                                                                                    Mismatches
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APPLICANT: Helen Jane Meadows
APPLICANT: Conrad Gerald Chapman
FITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30031-01
CURRENT APPLICATION NUMBER: US/09/828,746
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 09/236,080
PRIOR APPLICATION NUMBER: US 09/236,080
PRIOR FILING DATE: 1999-01-25
PRIOR APPLICATION NUMBER: ED 98300570.3
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: UK 9822135.1
PRIOR FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 6
SOPTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 6
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; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-6
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US-09-828-746-6
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Best Local Similarity 95.9
Matches 394; Conservative
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                                                                                  LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFG(^.,
                                                                                                                                                                              SNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFC (YALLGIPLFGFLLAGVGDQ 180
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US-09-655-272-4

Sequence 4, Application US/09655272
GENERAL INFORMATION:
APPLICANT: HONORE, ERIC
APPLICANT: FINK, MICHEL

14 Feb. 1

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RESULT 12
US-09-144-914-8
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NUMBER OF SEO ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 4
LENGTH: 370
TYPE: PRT
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Best Local Similarity
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APPLICANT: DUPRAT, FABRICE

TITLE OF INVENTION: MECHANOSENSITIVE MAMMALIAN POTASSIUM CHANNELS

TITLE OF INVENTION: ACTIVATABLE BY POLYUNSATURATED FATTY ACIDS AN

TITLE OF INVENTION: OF SAID CHANNELS IN DRUG SCREENING

FILE REFERENCE: 1383-00

CURRENT APPLICATION NUMBER: US/09/655,272

COURRENT FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: PCT/FR99/00404

PRIOR APPLICATION NUMBER: PCT/FR99/00404

PRIOR APPLICATION NUMBER: FR 98/02725

PRIOR APPLICATION NUMBER: FR 98/02725
EARLIER
EARLIER
                                                                                      TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS FILE REFERENCE: 989.6705CIP
                                                                                                                                       APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
                                                    CURRENT APPLICATION NUMBER: US/09/144,914 CURRENT FILING DATE: 1998-09-01
                  EARLIER APPLICATION NUMBER: 08/749,816 EARLIER FILING DATE: 1996-11-15
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NUMBER: 60/095,234
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96.7%;
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Pred. No. 1.7e-176;
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                                     SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 370
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GENERAL INFORMATION:
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Best Local Similarity
Matches 355; Conserv
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LENGTH: 370
                                                                                 TITLE OF INVENTION: NEW FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR TITLE OF INVENTION: CLONING AND THEIR USE, ESPECIALLY FOR THE SCREENING OF TITLE OF INVENTION: DRUGS
FILE REFERENCE: 1201-CIP2-00
CURRENT APPLICATION NUMBER: US/09/436,265
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR APPLICATION NUMBER: 60/095,234
PRIOR FILING DATE: 1996-08-04
PRIOR FILING DATE: 1996-11-09
PRIOR FILING DATE: 1996-11-09
PRIOR FILING DATE: 1996-13-09
PRIOR FILING DATE: 1996-13-09
PRIOR FILING DATE: 1996-13-09
PRIOR FILING DATE: 1996-13-09
                                                                                                                                                                                                                                                                    APPLICANT: LESAGE, FLORIAN
APPLICANT: FINK, MICHEL
APPLICANT: SALINAS, MIGUEL
APPLICANT: FARMAN, NICOLETTE
APPLICANT: LAZDUNSKI, MICHEL
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
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EARLIER APPLICATION NUMBER: FR 96/01565
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ORGANISM: Murine
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                                                                                                                                                                                                                                                                                                                                                                                                    8, Application US/09436265
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96.5%;
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Pred. No. 1.3e-175;
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CURRENT APPLICATION NUMBER: PCT/USO1/14965
CURRENT EILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
PRIOR TILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/206,526
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,033
PRIOR TILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,093
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/216,893
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/237,873
PRIOR FILING DATE: 2000-07-17
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PCT-US01-14965-73
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; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-436-265-8
: NUMBER OF SEQ ID NOS: 88
: SOFTWARE: PatentIn version
: SEQ ID NO 73
: SEQ ID NO 73
: LENGTH: 543
: TYPE: PRT
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Best Local Similarity
Matches 355; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Pharmacia & Upjohn Company
APPLICANT: Roberds, Steven L.
APPLICANT: Benjamin, Christopher
                                                                                          PRIOR APPLICATION NUMBER: 60/223,245 PRIOR FILING DATE: 2000-08-04
                                                                                                                             PRIOR FILING DATE: 2000-10-04
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; ORGANISM: Homo sapiens US-09-852-386-73
                                                                                                                                    PRIOR FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 60/207,092
PRIOR FILING DATE: 2000-05-25
PRIOR PPLICATION NUMBER: 60/206,526
PRIOR PPLICATION NUMBER: 60/207,033
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PRIOR APPLICATION NUMBER: 60/216,893
PRIOR PILING DATE: 2000-07-17
PRIOR PRIOR PRIOR PRIOR SATELY 2000-10-04
PRIOR APPLICATION NUMBER: 60/237,873
PRIOR PRILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 60/233,245
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: 60/223,245
PRIOR FILING DATE: 2000-08-04
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APPLICANT: Benjamin, Christopher
APPLICANT: Karnovsky, Alla M.
APPLICANT: Ruble, Cara L.
TITLE OF INVENTION: Human Ion Channels
FILE REFERENCE: 00133.US1
CURRENT APPLICATION UMBER: US/09/852,386
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/203,305
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Best Local Similarity 62.7%; Freu...
Matches 247; Conservative 54; Mismatches
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                                                                              SOFTWARE: PatentIn
SEQ ID NO 73
                                                                                                                     NUMBER OF SEQ ID NOS: 88
                                                          LENGTH:
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                                379 -SME------RRRLGLDQRAHSLDMLSP 399
                                                                   171 GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF 230
                350 LSAELAGNHNQELTPCRRTLSVNHLTNERDVLPP 383
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Search completed: August 28, 2001, 17:11:13 Job time: 602 sec

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                                                                                                                                                                                                                                                                                                                                                                                             Matches 410;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 1999-01-25
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                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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Pred. No. 5e-2.
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                                                                                                                                                                                                                  Sequence 4, Application US/09236080 Patent No. 6242217 GENERAL INFORMATION:
                               CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 107
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Best Local :
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                                                                                                                                           TITLE OF INVENTION: NO. FILE REFERENCE: GP30031
                                                                                                                                                                              APPLICANT: Helen Meadows APPLICANT: Conrad Chapman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/236,080 CURRENT FILING DATE: 1999-01-25
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APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compounds
FILE REFERENCE: GP30031
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ORGANISM: Homo sapiens
                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                   KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ
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Pred. No. 6.9e-200;
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                                                                                                         Query Match
Best Local Similarity
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                                                                                            Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 15-NOV-1996
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TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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STATE: PA
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109 AINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGN RTEGGKIFCIIYALLGIP 168
                                                          51 FLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFIS HSCVNSTELDELIQQIVA 108
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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215-875-8394
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98.1%;
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                                                                                          Mismatches 108;
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Best Local :
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Patent No. 555902
                                                                                                                                                                                                   Matches
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APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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   129
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Harrington, James J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                                                                                                                                                                                                  Local Similarity
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                                                                                              IVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                                                                                                               LLIFYISYLMFGAAIYYHIEHGEEKISRAEQRKAQIAINEYLLEELGDKNTTTQDEILQR 68
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                                                                 ISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNISPTTFAGRMIMIAYSVI 128
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                                                                                                                                                                                               Score 291.5; DB 1;
Pred. No. 2.8e-21;
4; Mismatches 123;
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Potassium Channel in Yeast
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US-08-332-312-4
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Patent No. 5559026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acid
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 201-831-3246
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                                                               132 RI----PAFLVLAILIVYTAFGGVLMSKLEPWSFFTSFYEGFITMTTVGFGDLMPRRDGY 187
                                                                                                                                                                                                                                                                                                                                                                                                     120 TSNQISH------WDLGSSFFFAGTVITTIGFGNISPRIL: KIFCIIYALLGIPLFGFL 173
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                                                                                                                                 205 KIRIISTIIFILFGCVLFVALPAIIFKHIEGWSALDAIY COTTLTTIGFGDYVAGGSDI 264
                                                                                                                                                                                                                                                                   297 TKDVGYLRRMLN-ELY 311
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CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                   TSNEVKKNAATETWTFSSSIFFAVTVVTTIGYGNPVPVTNIGRIWCILFSLLGIPL---T 71
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Pausch, Mark H.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barhanin, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,
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CORRESPONDENCE ADDRESS:
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ILECOMMUNICATION TOTAL
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CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/749,816 FILING DATE: 15-NOV-1996
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                                                                        PVGYGYIFPVSAYGRMCLIAYALLGIPLTLVTMADTGKFAAQLVT
                                                                                                          TIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGD---QLGTIFGKGIAKVEDTFIK 198
                                                                                                                                             ITSGIENSEQSIEIYTKKLILMLEDAHNAHAFEYFFLNHEIPKDMWTFSSALVFTTTTVI 148
                                  W----NVSQTKIRIISTIIFILFGCVLFVALPAI---IFKHIEGWSALDAIYFVVITLTT 251
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230 South Fifteenth Street, Suite 500
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Guillemare, Eri
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Lazdunki, Michel
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- IPAAIFV----CLLF-AYPLVVGFILCSTSNITYLDSVYFSLTSIFT
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24.3%;
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                                                                                                                                                                                                                                                                                                           Score 179; DB 3;
Pred. No. 4.4e-10;
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; MOLECULE TYPE:
US-08-749-816-3
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US-08-749-816-3
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Best Local Similarity
Matches 58; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08749816 Patent No. 6013470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08,
FILING DATE: 15-NOV-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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151 IAFKFEFGTFLAHF---LVVVSNRTRLAVKKAYYKLSQNFENAETPSNSLQHDYLIFLSS: 207
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                                                                   94 S---KLGKCLTKSSRIDGFGKAIFFSWTLYSTVGYGSLYPHSTLGRYLTIFYSLLMIPVF 150
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                                                                                                                                       44 ITLLVFNLIGAGIFYLAE-----TQNSSESLNENSEVSK -- CLHNLPIG----GKITAEMK 93
                                                                                                                                                                    52 LYVVLYLIIGATVEKALEQPHEISQRTTIVIQKQTFIS : SOVNSTELDELIQQIVAAIN 111
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                              -----FGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSUTKIRIIST-----IIFI-- 215
                                                                                                     AGIIPLGNTSNQISHWD-LGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPL- 169
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Lazdunki, Michel
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Pred. No. 3e
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LENGTH: 676
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Best Local
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APPLICANT: Keating, Mark T.
APPLICANT: Reating, Mark T.
TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
FILE REFERENCE: 2323-128
FILE REFERENCE: 2323-128
CURRENT APPLICATION NUMBER: US/09/135,021A
CURRENT FILING DATE: 1980-08-17
EARLIER APPLICATION NUMBER: 08/874,655
EARLIER APPLICATION NUMBER: 1997-06-13
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                                  341 QRATSIKRKLSAELAGNHNQELTPCRRTLSVNHLTNERDVLPP 383
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KKSVVVKKK---KFKLDKDNGVTPGEKMLTVPHITCD----PP
                                                                                                                                                                                           TLTTIGFGDYVAGGSDIEYLDFYKPVVWF------WILVGLAYFAAVLSMIGDW--LRV
                                                                                                                                                                                                                                                                      RIISTIIFI---LFGCVLFVALPAIIFK-------HIEGWSALDAIYFVVI
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US-09-135-021-80
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                                                                                                                                                                                                                                                                          RESULT
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EARLIER FILING DATE: 1997-05-13
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 80
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Patent No. 6150104
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                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Brant, Steven
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APPLICANT: Keating, Mark T.
TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN : 1 WHICH CAUSES JERVELL
TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROM: 5
TILE REFERENCE: 2323-128
CURRENT APPLICATION NUMBER: US/09/135,021A
CURRENT FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 581
                                    APPLICANT: Brant, Steven R.
APPLICANT: Yun, Chris C.H.
APPLICANT: Donowitz, Mark
APPLICANT: Tse, Chung-Ming
TITLE OF INVENTION: Cloning, Tissue Distril',
TITLE OF INVENTION: Functional Analysis Of,
TITLE OF INVENTION: HE3.
NUMBER OF SEQUENCES: 12
                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                  308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAG--
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Local Similarity 18.4%;
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  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF ( ----WILVGLAYFAAVLS | | | : : : : : : : : : : | |
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                                                                                                                                                                                                                                                                                                                                                                    RLSVEIYDKFQRATSIKRKLSAELAGNHNQELTPCRET VEHLTNERDVLPP 383
                                                                                                                                                                                                                                                                                                                                                                                                           ILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAA:NPDSSTWKIYIR----KAPRS
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Finnegan, Henderson, Farabow, Garrett &
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Washington

1300 I Street,

Suite

D.C.

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US-08-677-734A-9

Sequence 9, Application US/08677734A

Patent No. 5871919

Patent No. 5871919
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Best Local Similarity
"atches 76; Conserv?
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                                                                        GENERAL INFORMATION:
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                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
APPLICANT:
                 APPLICANT:
                                                                                                                                                                                                        305 AILAITFCGICCQKYVKANISEQSATTVRYTMKMLASGAET 345
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                                                                                                                                                                                                                                                                                    KGIVSFFVVSLGGTLVGV-IFAFLLSLVTRFTKHVRIIEPGFVFVISYLSYLTSEMLSLS 304
                                                                                                                                                                                                                                                                                                                    KPVVWFWI------LVGLAYFAAVLSMIGDW---LRVI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTPTLFFFYLLPPIVLDAGYFMPNRLFFGNL-----GTI--LLYAVIGTIWNAATTGLS 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---FHLSHKVTSVVPESALLI-------VLGLVLGGIV---WAADHIASFT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                      LYGVFLSGL----FLLFGSLIAAVDPVA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGSSFFF-----AGTVI-TTIGFGNISPRTEGGKIFCIIYALL----GIP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPLLALAVAVTSLRGVRGIEEEPNSGGSFQIVTFKWHHVQDPYIIALWILV--ASLAKIV 68
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Fordis, Jean B.
Fordis, Jean B.
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                                 Brant, Steven R
Yun, Chris C.H.
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                 Donowitz, Mark
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Chung-Ming
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19.0%;
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US-08-677-734A-10
; Sequence 10, Application US/08677734A
; Patent No. 5871919
; GENERAL INFORMATION:
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                                                                             RESULT 13
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Best Local Sim
Matches 73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                              103
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                                                                                                                              292 IISYLSYLTSEMLSLSAILAITFCGICCQKYVKANISECS YTTVRYTMKMLASSAET 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                       SFVALGGDNVTGVDCVKGIVSFFVVSLGGTLVGVV-FAFLLSLVTRFTKHVRIIEPGFVF 291
                                                                                                                                                                                                                                     DYVA-GGSDIEYLDFYKPVVWFWI-----LVGLAYFAAVLSMIGDW---LRVI-----
                                                                                                                                                                                                                                                                                                       IKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSAL-DAIYFVVITLTTIGFG 255
                                                                                                                                                                                                                                                                                                                                           ---GTI--LLYAVVGTVWNAATTGLSLYGVFLSGLMGDL(;135LLDFLLFGSLMAAVD---
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20005-3315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
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Pred. No. 0.19; %
                                                                                                                                                                -- SKKTKEEVGEFRAHAAEWTANVTAEFKET
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APPLICANT:

Brant,

Steven

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US-08-677-734A-12 ; Sequence 12, Application US/08677734A
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: FORDIS, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0043-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 834 amino acid
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Funct
TITLE OF INVENTION: NHE3.
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 IQQIVAAINAGIIPLGNTSNQISHWDLGSSFFF-----AGTVI-TTIGFGNISPR 151
                                                                                                                                                                                                                                                                                                                                                          141
                                                                                                                                                                                                                                                                                                                                                                                           152 TEGGKIFCIIYALL------GIPLFGFLLAG-VGD-QLG----TIFGKGIAKVEDTF 196
                                                                                                      292 IISYLSYLTSEMLSLSAILAITFCGICCQKYVKANISEQSATTVRYTMKMLASSAET
                                                                                                                                                                                                                            256 DYVA-GGSDIEYLDFYKPVVWFWI-----LVGLAYFAAVLSMIGDW---LRVI----- 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                     90 ---VLGLVLGGIV---WAADHIASFTLTPTVFFFYLLPPIVLDAGYFMPNRLFFGNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 EWAHVQDPY-VIALWILVASLAKIGFHLSHKV---TSVVPESALLI-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 KWKTVSTIFLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDEL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                   SFVALGGDNVTGVDCVKGIVSFFVVSLGGTLVGVV-FAFLLSLVTRFTKHVRIIEPGFVF
                                                                                                                                                                                                                                                                                                           IKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHIEGWSAL-DAIYFVVITLTTIGFG 255
                                                                                                                                                                                                                                                                                                                                                    ---GTI--LLYAVVGTVWNAATTGLSLYGVFLSGLMGDLQIGLLDFLLFGSLMAAVD---
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                                                                                                                                                                                                                                                                   ----PVAVLAVFEEVHVNEVLFI----IVF----GESLLNDAVTVVLYNV----FE 232
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                                                                                                                                             SKKTKEEVGEFRAHAAEWTANVTAEFKET 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Na+/H+ Exchanger Isoform
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Fordis, Jean B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: FOZÓIS, JEAN B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                  277
                                                                                                                                                                                                                                           139 L-----GSI--LLYAVVGTVWNAATTGLSLYGVFLSGI---
                                                                  295 W---LRVI---
                                                                                                   225 VLYNVFQSFVTLG-GDKVTG-----VDCVKGIVSFFVV.
                                                                                                                               241 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI
                                                                                                                                                                                                       199 WNVSQTKIRIISTIIFILFGCVLFVALPA-----
318 TANVTAEFKET 328
                                                                                                                                                                                                                                                                          148 ISPRTEGGKIFCIIYALL------GIPLFGFLLAGVGDOLGTIFGKGIAKVEDTFIK 198
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                                                                                                                                                          --MGELKIGLLD---FLLFGSLIAAVDPVAVLAVFEEN
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                                FTKHVRVIEPGFVFIISYLSYLTSEMLSLSSILAITFCG (*
                                                                                                                                                                                                                                                                                                                                              LDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFF------AGTVI-TTIGFGN 147
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1300 I Street, N.W., Suite 700
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Chris C.H.
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19.7%; Pred. No. 0.31;
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al Analysis Of the Human Na+/H+ Exchanger Isoform,
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                                                                                                                                                                       CVLFITVFGESLLNDAVTV
                                                                                                    "STLVGVV-FAFLLSLVTR 276
                                                                                                                                                                                                                                                                                                                                                                                                                 VIQKOTFISQHSCVNSTE
                                PKYVKANISEQSATTVRY 336
                                                                  SKKTKEEVGEFRAHAAEW 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 832;
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337 TMKMLASGAET 347

US-08-720-484A-5

Sequence 5, Application US/08720484A Patent No. 5990281

GENERAL INFORMATION:

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; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1036 amino acids
; TYPE: Amino Acid
TOPOLOGY: Linear
US-08-720-484A-5
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Best Local Similarity
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APPLICATION NUMBER: US/08/720,484A
FILING DATE: 30-Sep-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1050
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                           396
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                          282 LAYFAAVLSMIGDWLRVISKKT-KEEVGEFRAHAAEWTANVTAEFK--ETRRRLSVEIYD 338
                                                                                 502 EW-AQSFRQFIICKISSV-FEEKSSCRIENRPSVGVLQLHLLCLFSSGIVMSTWCW----
                                                                                                                                                                                                                   189
                                                                                                                                                                                                                                                                                                     140
                                                                                                                                                                                                                                                                                                                                                                                  101 ELIQQIVAA---INAGII-------PLGNTSNQISHWDLGSSFFFAG-----TV 139
                                                                                                                                                                                                                                                                                                                                                                                                                            281
                                                                                                                                                                       446 MVMLFGLKHFANDIKSTSASNKIHLIIMRMGVCALLTLVFIL----VAIACHVTEFRHAD
                                                                                                                                                                                                                                                                                                                                             338 SCIVIFVLVYYFLTAGMVWFVFLTYAWHWRAMGHVQDRID--KKGSYFHLVAWSLPLVLT 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1 DNA Way
CITY: South San Francisco
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                                                                                                                           GWSALDAIYFVVITLTTIGFGDYVA------GGSDIEYLDFYKPVV----WFWILVG
----TPSSIETWKRYIRKKCGKEVVEEVKMPKHKVIAQTWAKRKDFEDKGRLSITLY- 608
                                                                                                                                                                                                               IA-----KVEDTFIKWNVSQTKIRII-----STIIFILFGCVLFVALPAIIFKHIE
                                                                                                                                                                                                                                                           ITTMAFSEV----DGNSIVGICFVGYINHSMRAGLLLG-PLCGVILIG-----GYFITRG
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Rosenthal, Arnon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.6%; Score 96.5; DB 2; Length 1036; 21.8%; Pred. No. 0.54; ative 53; Mismatches 154; Indels 131;
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Search completed: August 28, 2001, 17:06:21 Job time: 525 sec

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Copyright (c) 1993 - 2000 Comp
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Human potas	potassium channel		(+Hn	K+Hnov59.		
Potassium channel; cardiovascular dis	=	el; ataxia; disorder; C	9	arrhythmia; NS disorder;	epilos Bart	Bartter's syndrome; rder.
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Homo sapiens	ns.					

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19-JAN-1999;
25-FEB-1998;
07-AUG-1998;
            WPI; 1999-527591/44.
N-PSDB; AAZ11915.
                        Curran
                                                                  02-SEP-1999.
                                (AXYS-) AXYS PHARM INC.
                                                          22-FEB-1999;
                                                                          W09943696-A1
                        ME,
                        Hu P,
                                        99US-0116448.
98US-0076687.
98US-0095836.
                                                         99WO-US03826
                        Miller
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New nucleic acids encoding mammalian K+Hnov por issium channel proteins, useful for the diagnosis and treatment of episodic

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Best Local
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                                      AAY28496;
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 12-OCT-1999
                                                                          AAY28496 standard;
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Pred. No. 1.9e-209;
1; Mismatches 0;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chapman CG, Meadows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1998;
27-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-1998;
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                                                                    aiyfvvitlttigfgdyvaggsdieyldfykpvvwfwil. Hayfaavlsmigdwlrvis
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ELTPCRRTLSVNHLTNERDVLPPLLKTESIYLNGLTPHCAGEEIAVIENIK
                      kktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsikrklsaelagnhnq
                                                                                           AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILV ;LAYFAAVLSMIGDWLRVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Page 24; 44pp; English.
                                                                                 pore potassium channel used for, e.g. treatment of cancer,
ry, cardiovascular and inflammatory diseases
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98EP-0300570
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Best Local Similarity
                                                                                                                                                                                                                                                                                                  2P domain potassium channel family of protests which play a part in the control of resting membrane potential. Modulation of these channels will therefore affect neuronal excitability, thereby leading to a modulation of neurotransmitter release and activity of neuronal networks. Such modulation therefore may be useful for the treatment of certain neurological conditions such as anilarcom.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; TREK; 2P domain potassium channel; resting membrane potential; neuronal excitability; neurotransmitter release modulation; epilepsy; neurological disorder; sleep-related disorder; cognitive dysfunction; attention deficit disorder; addiction; anxiety; phobia; parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;
                                                                                                                                                                                                                                                        neurological conditions such as epilepsy, sleep-related disorders, cognitive dysfunction, attention deficit disorder, addiction, anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy, incontinence, erectile dysfunction or alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of human TREK1 polypeptide, polynucleotides encoding them and modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related disorders, addiction and dyskinesias including Parkinson's and Huntington's chorea
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erectile dysfunction; alopecia.
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                                                                                                           maapdlldpksaaqnskprlsfstkptvlasrvesdttinvmkwktvstiflvvvlylii
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Pred. No. 1
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1.9e-209;
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1 MAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVESDTTIMVHKKTVSTIFLVVVLYLII

Query Match Best Local Matches

Similarity

96.9**%**; 95.9**%**;

Score 2035; Pred.

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12;

Mismatches No.

3.4e-203; nes 5; DE 20:

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             This sequence is the mouse h-TREK1 polypept! . encoded by the h-TREK1 polypucleotide AAZ00040. h-TREK1 is a two per potrassium channel. The polynucleotide sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptides. The methods of diaments may be used in the treatment of diseases including cancer, puln cary, cardiovascular, and inflammatory diseases including cancer, polin cary, cardiovascular, and schizophrenia, neurodegenerative diseases including Alzheimer's, stroke, and head trauma and neurological dispreces including migraine.
                                                                                                                                                                                                                                                                                                                                                         h-TREK1; two pore potassium channel; inflamma .ry disease; chromosome 1q32.
                                                                                                                                                                                                       Chapman
                                                                                                                                                                                                                                              09-OCT-1998;
27-JAN-1998;
Sequence
                                                                                                                                                    New two
                                                                                                                                                                                   WPI; 1999-469126/39
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                                                                                                                                          pore potassium channel used for, e.
ry, cardiovascular and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                     Page 26; 44pp; English.
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                            The present sequence represents a mechanically sensitive potassium channel protein designated TREK-1. The protein is activated by polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nerve systems in humans and animals, e.g. epilepsy, cardiovascular disease (arrhythmia), neurodegeneration (particularly where associated with
                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                    New mechanically sensitive potassium channel, use specific modulators, potential therapeutic agents system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         muscular disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sensitive potassium
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disease; epilepsy; cardiovascular disease; arrhythmia;
on; ischemia; anoxia; hormone secretion abnormality;
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heart and
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AX Huma
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KW 2P d
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Best I
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        WPI; 2000-365583/31
N-PSDB; AAA27105.
                                  Chapman
                                                                      03-NOV-1998;
07-OCT-1999;
                                                                                                                                                                     Human; h-TRAAK; potassium channel polypeptid
2P domain potassium channel; neurodegenerati:
psychiatric disorder; neurological disorder; "
                                                                                                                                                                                                                                             AAY94425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ischemia or anoxia), abnormalities of hormone secretion and muscular disease. The protein itself may be used to treat these diseases. Antibodies specific for the protein are used to detect it in tissues also as therapeutic inhibitors or activators.
                                                                                                 03-NOV-1999;
                                                                                                                                   WO200026253-A1
                                                                                                                                                                                                        Human h-TRAAK polypeptide
                                                                                                                                                                                                                                                              AAY94425 standard;
                                                                                                                                                     Homo sapiens
                                                    (SMIK )
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99GB-0023668
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96.7%;
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Pred. No. 3
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                                                                                                                                                                                disease;
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AAY9442

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Best Local Similarity
Matches 145; Conserv
                                                               03-NOV-1998;
07-OCT-1999;
                                                                                                                                                       03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                        Human; h-TRAAK; potassium channel polypeptide; 2P domain potassium channel; neurodegenerative disease; stroke; psychiatric disorder; neurological disorder; Gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY94426 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    schizophrenia, neurodegenerative disease including Alzheimer's, s
and head trauma and neurological disorders including migraine and
epilepsy. The present sequence is human h-TRAAK protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   imbalance and for identifying agonists and antagonists of h-TRAAK polypeptides and polynucleotides may also polypeptides. The h-TRAAK polypeptides and polynucleotides may also be useful for treatment and prevention (e.g. as veccines) of certain diseases, such as pain, psychiatric disorders including depression of the diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK polynucleotides from human tissue samples. h-TRAAK polypeptides have homology to the 2P domain potassium channel fam polypeptides. The h-TRAAK polypeptides and polynucleotides may be used in diagnostic assays for conditions related to h-TRAAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated h-TRAAK polypeptides belonging to the potassium family of polypeptides, useful for the diagnosis and treatment h-TRAAK related disorders, e.g. depression and schizophrenia -
                                                                                                                                                                                                                                                                            WO200026253-A1
                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human h-TRAAK polypeptide #2
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(SMIK ) SMITHKLINE
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Pred. No. 5.2e-75;
1; Mismatches 76;
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                                                                                                                          polyunsaturated fatty acid; arachidonic acid: iluzole; heart disease; nervous system disease; epilepsy; cardiovasculur disease; arrhythmia; neurodegeneration; ischemia; anoxia; hormone : cretion abnormality:
                                                                                                                  muscular
                                                                                                                                                                                                                                                                       A mechanically sensitive potassium channel pro ein TRAAK.
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                                                                                                                                                                                                                                                                                                                                                                          AAY30647;
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DB; AAA27106.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a mechanically sensitive potassium channel protein designated TRAAK. The protein is activated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mechanically sensitive potassium channel, used to 
specific modulators, potential therapeutic agents for 
system disorders
                                 chromosome 1q32.
                                                 partial h-TREK1; two pore potassium channel;
                                                                                Partial h-TREK1
                                                                                                               12-OCT-1999
                                                                                                                                                                            AAY28498 standard; Protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                      LVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTA 323
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                                                                                                                                                                                                                                                                                                                                                                                 cifyalvgiplfgmllagvgdrlgsslrrgighieaiflkwhvppglvrslsavlfllig
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                                                                                                                                                                                                                                                                                                                                                                                                                                            fikllvealggganpetswtnssnhssawnlgsafffsgtiittigygnivihtdagrlf 120
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                                                                               polypeptide.
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49.8%;
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Pred. No. 3e-72;
7; Mismatches 83;
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heart a
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                                                   disease;
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Best Local Similarity
Human; TWIK-3; TWIK-4; TWIK-2; central nervous system disorder; demen Trandem of p domains in a Weak Inward rectifying K+ channel; epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis; depress amyotrophic lateral sclerosis; progressive supranuclear palsy; mania; Creutzfeldt-Jacob disease; psychiatric disorder; schizophrenic disord Korsakoff's psychosis; anxiety disorder; phobic disorder; amnesia;
                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide AAZ00041. AAZ00039 and AAY284. The complete h-TREK1 polynucleotide and polypeptide sequences. h-7-3-31 is a two pore potassium channel, and the gene maps to humar promosome 1932, between the markers D1S237 and W15105. The polynuclei de sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK1 polypeptides. The methods of diagnosis may be used in the treatment of diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, palso, psychiatric disorders including Alzheimer's, stroke, and head trauma and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New two pore potassium channel used for, e.g pulmonary, cardiovascular and inflammatory d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is a partial h-TREK1 polypeptical encoded by the h-TREK1 polynucleotide AAZ00041. AAZ00039 and AAY284 are complete h-TREK1
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27-JAN-1998;
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                                                                                      Human TWIK-2 protein
                                                                                                                04-DEC-2000
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                                                                                                                                                                                                                                           DQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILEGCVLEVAL 225
                                                                                                                                                                                                                                                                            dqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfval 107
                                                                                                                                                                                                                                                                                                                                 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Page 25;
                                                                                                                                                                                                                                                                                                                                                                                                                      including migraine.
                                                                                                                                                                                                                                                                                                                                                                                             107
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                                                                                                              (first entry)
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98EP-0300570
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Pred. No. 3.
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disorder;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   memory loss), neurological disorders (e.g. migraine), obesity, and cardiac disorders. The nucleic acids, proteins, protein homologues and antibodies against them may be further used in screening assays, predictive medicine. The nucleic acids can be inserted into vectors and predictive medicine. The nucleic acids can be inserted into vectors and used as gene therapy vectors, to express TWIK protein, to detect TWIK mRNA, modulate TWIK activity, and screen for drugs or compounds that modulate TWIK activity. Host cells may be used to produce non-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease), psychiatric disorders (e.g. depression, schizophrenic disorders, Korsakoff's psychosis, mania, anxiety disorders or phobic disorders), learning or memory disorders (e.g. amnesia or age-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and therapeutic agents for potassium channel associated disorders, e.g. central nervous system disorders (e.g. Alzheimer's disease, dementia, Parkinson's disease, multiple sclerosis, amyotrophic lat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TWIK-2 (Tandem of P domains in a Weak Inward rectifying potassium (K+) channel-2), TWIK-3 and TWIK-4 nucleic acids and proteins are useful as targets for developing modulating agents to regulate a variety of cellular processes. They may be useful for developing novel diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dementia, Parkinson's uisease, muiting, epilepsy, Creutzfeidisclerosis, progressive supranuclear palsy, epilepsy, Creutzfeidisclerosis, schizophrenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 148pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New tandem of P domains in a weak inward rectifying potassium channel proteins and genes for e.g. developing therapeutic agents for potassium channel associated disorders, e.g. central nervous system, psychiatric disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-572183/53.
N-PSDB; AAA37770, AF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2000; 2000WO-US05409
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neurological disorder; cardiac disorder; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200052164-A2
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                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                       114 IIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFL 173
                                                                                                                                                                                                                                                                                                                                                                         72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 VVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRLSVEIYDKFQRATSIKRKLSA
                                                                                                                                                                                                                 ltwi-salgkffggrakrlgqfltkrgvslrkaqitctvifivwgvlvhlvippfvfmvt
                                                                                                                                                                                                                                                                                         LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iifylaigaaifevleephwkeakknyytqklhllkefpclgqegldkilevvsdaagqg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents the human TWIK-2 protein of the invention.
                                                                    egwnyieglyysfitistigfgdfvagvnpsanyhalyryfvelwiylglaw----lslf
                                                                                                                                            EGWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAYFAAVLSMI 292
                                                                                                                                                                                                                                                                                                                                                             vaitgnqt--fnnwnwpnamifaatvittigygnvapktpagrlfcvfyglfgvpl---c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 499 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 427; DB 21;
Pred. No. 9.9e-36;
0; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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   352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                 TASKI (see AAY79674). TASK2 is a unique pot assium transport channel that is regulated by external pH, and is probability expressed in kidney and epithelial tissues. The invention relates to: identification of the native renal channel. In the properties of TASK2; identification of potent pharmacology that specifically modulates the activity of the TASK-2 channel; localizing K+ channels comprising the TASK2 subunit in viv; and the generation of mice in which the TASK2 gene has been in jointeed. The invention
                                                                                                                     The present sequence is that of human TASK2 (TWIK-related acid-sensitive potassium channel 2), a novel member of the 2P domain potassium channel family that also includes WIK-1 (see AAY79673) and
                                                                                                                                                                                                New nucleic acid encoding a non-inactivating outwardly rectifying potassium transport channel, designated TASK: useful in the treatment of hypertension or dysfunctions of the kidner. Liver or pancreas -
                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                     WPI; 2000-376487/32.
                                                                                                                                                                                                                                                                                              Duprat F,
                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TASK2; TWIK-related acid-sensitive K+ channer 2; potassium channel; drug screening; hypertension;
                                                                                                                                                                                                                                                                                                                                                08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                            09-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               18-MAY-2000
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                                                                                                                                                                                                                                                                                                                       (CNRS ) CNRS
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                                                                                                                                                                           Fig 14a; 91pp;
                                                                                                                                                                                                                                                                                            Lesage F,
                                                                                                                                                                                                                                                                                                                        CENT NAT RECH SCI
to diagnostic tests and therap ic methods to: detect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transplant rejection; therapy; diagnosis
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99US-0436265
                                                                                                                                                                                                                                                                                                                                                                                      99WO-IB01886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "P domain"
77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "transmembrane 113..133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-glycosylated"
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                                                                                                                                                                           English.
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24-JUL-1998;
07-AUG-1998;
25-AUG-1998;
09-SEP-1998;
29-SEP-1998;
                                                                                                                                                                                                                                             cytokine production; cell proliferation; cell differentiation; immune deficiency; infectious disease; autoimmune disorder; asthma; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; allergic reaction; osteoporosis; osteoarthritis; periodontal disease; nervous system disorder; Alzhelmer's disease; Parkinson's disease; Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury; systemic cytokine damage; tissue differentiation; contraceptive; stroke; coagulation disorder; myocardial infarction; inflammatory condition; septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pancreas and/or liver dysfunctions that may arise from mutat
the TASK2 gene; protect against tissue rejection in kidney,
and liver transplants; and identify potential drugs capable
modulating TASK2 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and treat human pancreas and/or
                                                                                                       22-JUL-1999;
                                                                                                                                         03-FEB-2000
                                                                                                                                                                         WO200005367-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 VVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKHI 23:
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                                                                                                                                                                                                                                                                                                                                                                                                protein; hydrophobic domain; nutritional source; haemato
ine production; cell proliferation; cell differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone HP10538
                 98JP-0208820.
98JP-0224105.
98JP-0238116.
98JP-0254736.
                                                                                                       99WO-JP03929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypertension and diseases associated with kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.3%; 31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
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Pred. No. 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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9.9e-36;
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of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    conditions such as asthma, and in immune suppression after organ
conditions such as asthma, and in immune suppression after organ
conditions such as asthma, and in immune suppression after organ
conditions such as asthma, and in immune suppression of haematopoiesis
and consequently in the treatment of myloid cell
conditions. It is also used in composition or lymphoid cell
conditions and in the treatment of prodontal disease and other
conditions for processes. The protein is used
conditions disease. The protein is used
the treatment of osteoporosis
conditions disease. They are useful for protection or regeneration and
treatment of lung or liver fibrosis, reperful contoning they are
also used for promoting or inhibiting tissue. Efferentiation. They are
also used for promoting or inhibiting tissue. Effect and and activities and as a fertility inducing there is contraceptives since they exhibition or inhibit or
treating various coagulation disorders and in reactions. They are used for
the protein is also used in the conditions of the conditions resulting from coagulation activities e.g. myocardial
conditions resulting from coagulation activities. They are used to
inhibitors or agonists of receptor/ligand in reactions. They are used to
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 106; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               potential genetic disorders. The DNA and pro in can also be used as nutritional sources or supplements. The prot exhibits cytokine, cell proliferation, cell differentiation activitie, and induces production of other cytokines in certain cell populations. The protein also exhibits immune stimulating or immune suppressing activity. It can be used in the treatment of various immune deficiencies and disorders, and to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human proteins having hydrophobic doma seeful for osteoporosis, Alzheimer's disease, Parkinson states, ast multiple sclerosis, rheumatoid arthritis, casses, anaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SAGA )
(PROT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid arthritis. It is also useful in the treatment of allergic reactions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 245-247; 351pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          treat inflammatory conditions such reperfusion injury, arthritis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infections The protein is also used for treating autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic marker. The protein can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hydrophobic
                                                                                                                                                                                                                                                                                                                                                                                                          prevent tumours.
                    186
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                                                                                                                                                                                                                                                       54 VVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQH.
iifylaigaaifevleephwkeakknyytqklhllkeir
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31.1%;
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Pred.
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                                                   e.g. central nervous system disorders (e.g. Alzheimer's disease, dementia, Parkinson's disease, multiple sclerosis, amyotrophic lateral sclerosis, progressive supranuclear palsy, epilepsy, Creutzfeldt-Jacob disease), psychiatric disorders (e.g. depression, schizophrenic disorders, Korsakoff's psychosis, mania, anxiety disorders or phobic disorders), learning or memory disorders (e.g. amnesia or age-related memory loss), neurological disorders (e.g. migraine), obesity, and cardiac disorders. The nucleic acids, proteins, protein homologues and antibodies against them may be further used in screening assays, predictive medicine. The nucleic acids can be inserted into vectors and used as gene therapy vectors, to express TWIK protein, to detect TWIK mRNA, modulate TWIK activity, and screen for drugs or compounds that modulate TWIK activity. Host cells may be used to produce non-human
                                                                                                                                                                                                                                                                                                                       This sequence represents the human TWIK-3 protein of the invention. The TWIK-2 (Tandem of P domains in a Weak Inward rectifying potassium (K+) channel-2), TWIK-3 and TWIK-4 nucleic acids and proteins are useful as targets for developing modulating agents to regulate a variety of cellular processes. They may be useful for developing novel diagnostic and therapeutic agents for potassium channel associated disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tandem of P domains in a weak inward rectifying potassium channel proteins and genes for e.g. developing therapeutic agents for potassium channel associated disorders, e.g. central nervous system, psychiatric
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Fig 3; 148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
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Luo Y, Gendreau SB,
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                                                             WPI; 2001-159864/16.
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                                                                                                         Gillett LA,
SB, Jacobus
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Pred. No. 3.
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DA, Tietjen
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                                                                                                         Winslow JW;
Jeschke P;
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New tandem pore domain weak inward rectifyi whotassium

ion (TWIK)

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RESULT 1
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ID AAW2
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                                                                                     08-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TWIK-1
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                                                                                                                                                                                                                                                            14-AUG-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWIK-1 potassium channel; screening; Tandem of P domains in a Weak Inward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW23397 standard;
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| 284 mmltltvfyd 293
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Pred. No. 3e-31;
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rectifying K+; antibody.
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Best Local S
Matches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for modulating activity of TWIK-1 type channels may also be useful therapeutically, e.g. for control of epilepsy, arrhythmia, vascular disease, neurodegeneration (particularly of is haemic or anoxic origin), endocrine or muscular disorders. The cDNA and the vectors can also be used to create transgenic animals (especially knock-out animals) for use as models of TWIK-1 related diseases. Analysis of the sequence of the TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies can be used to detect TWIK-1 channels and for inhibiting or activating the channels in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a protein califrising a potassium chann with the properties of a TWIK (Trandem of p.3. mains in a Weak Inward rectlifying K+)-1 channel. This is the first represent of a new family of channels consisting of 4 transmembrane segments and two p domains, and being only weakly rectlifying. The cDNA, vectors, the cells expressing TWIK-1 type channels and the protein are used to compensate for deficiency of potassium channels in various tissues. Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid encoding new potassium channel disignated TWIK-1 - useful for treating channel deficiency diseates, screening for active agents and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Lesage F, !
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                                                                                                                                                                                                                                   AINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNI: RTEGGKIFCIIYALLGIP 168
                                                                    aavfsvleddwnflesfyfcfislstiglgdyvpgegynqkfrelykigitcylllglia
                                                                                                         ATIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAY
                                                                                                                                                                              LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTII--FILFGCVLFVALP
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Pred. No. 4.9e-
62; Mismatches
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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inward rectifier potassium channel TWIK-1 - humar C;Species: Homo sapiens (man) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 C;Accession: S65566

R;Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F EMBO J. 15, 1004-1011, 1996

azdunski, M.; Romey, G.; Barhani

#rext_change 05-Nov-1999

A;Molecule type: mRNA A;Residues: 1-336 <LES> A;Cross-references: EMBL:U33632; NID:g1086490; PIDN:AAB01688.1; PID:g1086491

A;Title: TWIK-1, a ubiquitous human weakly inward worthfying K(+) channel with a nove A;Reference number: \$65566; MUID:96183184
A;Accession: \$65566
A;Status: preliminary

RESULT S65566

probable potassium channel chain n2P38 - Caenori C;Species: Caenoriabditis elegans C;Date: 21-Jan-2000 #sequence_revision 21-Jan-20 C;Accession: T43509 R;Wang, Z.W.; Salkoff, L. submitted to the EMBL Data Library, August 1998 A;Description: Potassium channels in C. elegans RESULT T43509 밁 Q 밁 Qy В Qy DЬ Ş A; Reference number: Query Match
Best Local Similarity Matches 144 109 260 200 285 FAAVLSMIGDWLRVISK-----KTKEEVGEFRAHAAE 85 25 51 FLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTF:SQHSCVNSTELDELIQQIVA 108 AINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISFRTEGGKIFCIIYALLGIP 168 MLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE AIIFKHIE-GWSALDAIXFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAY FTLLFLTAVVQRITVHVTR---RPVLYFHIRWGFSKQVVA(VHAVLLGFVTVSCFFFI--P LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKI: ISTII--FILFGCVLFVALP ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGH: VPLSDGGKAFCIIYSVIGIP AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKI:RELYKIGITCYLLLGLIA FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLE 90; Conservative Z22450 18.1%; 62; Score 379.5; Pred. No. 3.6e 52; Mismatches 21-Jan-200 Caenorhal sitis elegans 5; E2 2; 3.6e-23; nes '08; 295 text_change 21-Jan-2000 Indels 17; Length Gaps 199 84 9;

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outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T32347 R;Murray, J; Wohldmann, P.; O'Neal, D. submitted to the EMBL Data Library, September 1997 A;Description: The sequence of C. elegans cosmid F34D6. A;Reference number: Z21153 A;Reference number: Z21153 A;Accession: T32347 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-336 <MUR> A;Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.3 A;Experimental source: strain Bristol N2; clone F34D6 C;Genetics: A;Gene: twk-23; CESP:F34D6.3 A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-329 <WAN>
A; Cross-references: EMBL: AF083652; PIDN: AAC32863.1
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RTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIIS
                                                                                                                                                                                                                                                 MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQ-----RTTIVIQKQTFISQHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GWGGLLIFGGAFMFSSYENWTYFDAVXYCFVTLTTIGFGDYVALQKRGSLQTQPEYV-FF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTEL 99
                                                                      MTDAGKVFCMLYALAGIPLGLIMFQSIGERMNTFAAKLL----RFIRRAAGKQPIVTSS
                                                                                                                                            MSNA-DYETLEATIVKSVPHKAGY------OWKFSGAFYFATTVITTIGYGHSTP 108
                                                                                                                                                                             CVNSTELDELIQQIVAAI--NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISP 150
                                                                                                                                                                                                                MKRQNIRTLSLIVCTLTYLLVGAAVFDALETENEILQVRGLGEPRKLVQRVREKLKTKYN
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33.7%;
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Pred. No. 2.1e-20;
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hypothetical protein K01D12.4 - Caenorhabditis e/
C;Speciles: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-19.
C;Accession: T23182
R;Dobson, R.
A; Experimental source: C; Genetics:
                                     A;Residues: 1-383 <WIL>
A;Cross-references: EMBL:Z75543;
                                                                                                             submitted to the EMBL Data A; Reference number: Z19703 A; Accession: T23182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      potassium channel protein - fruit fly (Drosophila :lanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-199 #text_change 17-Nov-2000
C;Accession: T13807
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A;Map position: 1
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                                                                                           from
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Pred. No. 1e-17
                                                                                                                                                    June
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                                                                                             GB/EMBL/DI
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                                       :PDB:
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                                         CESP: K01D12.4
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1. The ...

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RESULT 6
T19860
hypothetical protein C40C9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to
C;Accession: T19860
R;Hembry, C.
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A; Residues: 1-334 <W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: Z19188
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A; Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2
                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: CESP:C40C9.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated
                                                                                                                                                                                                                                                                                           Matches
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Best Local Similarity
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                                 CVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYV--AGGSDIEYLDFYKPVVWF
                                                                     GVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLTIGFMV--
                                                                                                                                                                 VAAINAGIIPLGNTSNQISH-WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                                                                                                                                                                                                                              IFLVVVLYLIIGATVFKALEQPHEISQRTTIV----IQKQTFISQHSCVNSTELDELIQQI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACFFYCLSNVSSIVVRQLLNWM---IKKMDVKV-EDRSFLC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAYF-----AAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSV 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TASAGIYSVVENWNYIDSLYFCFISFATIGFGDYVSNQQDVTRMSPDLYRFVNFCLLTLG
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----IVSGTYMFHTIEKWSIFDAYYFCMITFSTIGFGDLVPLQQVNALQDQPLYVFATIM 233
                                                                                                       GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIK-----WNVSQTKIRIIS-TIIFILFG
                                                                                                                                              IA-----IKSIPQQAGYQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLFCMIFALF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYL--DFYKPVVWFWILVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SATVISTIGFGTSTPRTHLGRFITIVYGVVGCTCCVLFFNLFL----ERLVTGMSYILRS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTVITTIGFGNISPRTEGGKIFCIIYALLG----IPLFGFLLAGVGDQLGTIFGKGIAK 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AIDNRMADYQKVYCKHKPLNECDFEEMVRFISDGATSGLL-----NSRSRFDHLGSLFF 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TI---VIQKQTFISOHSCVNSTELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFF 135
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                                                                                                                                                                                                                                                                                                                                                                                  60/2; 98/1; 145/3; 160/3; 181/1;
                                                                                                                                                                                                                                                                                          Conservative
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23.6%;
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                                                                                                                                                                                                                                                                                          Score 284.5; DB:
Pred. No. 1.7e-15
3; Mismatches 11:
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Pred. No. 1e-15;
0; Mismatches 1
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C;Date: 11-Jan-2000 #sequence_review.
C;Accession: 743361
R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, Aug
A;Description: Potassium channels in C.
A;Reference number: 222450
A;Accession: 743361
A;Accession: 743361
                                                       A; Accession: T43394
A; Status: preliminary; translated
                                                                                         R;Kunkel, M.T.; Salkoff, L. submitted to the EMBL Data Library, A;Description: Potassium channels in A;Reference number: 222479
                                                                                                                                                                       potassium channel chain n2P18 homolog - Caenorhabditis elegans C;SpecLes: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_chang.C;Accession: T43394
                 A; Molecule type: mRNA
A; Residues: 1-461 < KUN>
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A; Residues: 1-364 <WAN>
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C; Species: Caenorhabditis elegans
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 IFLVVVLYLIIGATVFKALEQPHEISQRTTIV---IQKQ1F1SQHSCVNSTELDELIQQI 106
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EMBL: AF083650;
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Pred. No. 1.
                                                         from GB/EMBL/DD3J
 PIDN:AAC32861
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                                                                                                                 August 1998
n C. elegans
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1 C. elegans.
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hypothetical protein T28A8.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T25392 R;Lloyd, C.
                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:Z92813; P:
A;Experimental source: clone T28A8
C;Genetics:
A;Gene: CESP:T28A8.1
A;Map position: 3
A;Introns: 73/1; 112/3; 179/2; 209,
                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, Mar
A; Reference number: Z20027
A; Accession: T25392
A; Status: preliminary; translated from
A; Molecule type: DNA
A; Residues: 1-393 <WILD
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Best Local
 124
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                                                                                                                                                 44 WKTVSTIFL------VVVLYLIIGATVFKALEQPHEISQRTTIV----IQKQTFIS---
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                                                                                                                                                                                                                Local Similarity
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                                AGTVITTIGEGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGD-----QLGTIFGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TNERDVLPPLLKTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PIVGVLLLIGLSLVSTVMTLIQQQIEALASGMKDNIDQEYARALNEAREDGEVDEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---TIIFILEGCVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102;
TTTLLTTIGYGNLTPVTGRGKLLCILYALFGVPLILITVADIGKFLSENIVQLYTWYRKL
                                                                  EMRESGIGQHVVEDLAVKYVDNVTRILFEAFDTHCIGAKHLRPGGEDEDYNWTYMTALFF
                                                                                                --QHSCVNSTELDELIQQIVAAINAGIIPLGNT------
                                                                                                                                WKTYARIILAHVSLIVLSVVYVGFGAFLFYQLEQPNEVEVRARNIERFNIHKRQMIEHLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -TDNDLLETLIREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHA-----AEWTAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STELDELIQQIVAAIN------
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                                                                                                                                                                                                 81;
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                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                 179/2; 209/3;
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23.5%;
                                                                                                                                                                                                               13.3%; Score 279; DB 2; 27.0%; Pred. No. 5.7e-15;
                                                                                                                                                                                                 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68;
                                                                                                                                                                                                                                                                                                                                                               PIDN:CAB07286.1; GSPDB:GN00021; CESP:T28A8.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 282.5; DB 2; Pred. No. 3.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              March 1997
                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                 287/2;
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                                                                                                                                                                                                                                                                                 310/3;
                                                                                                                                                                                               107;
                                                                                                                                                                                                                            Length 393;
                                                                                                                                                                                              Indels
                                                                                               SNQISHWDLGSSFFF 135
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                                 188
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 183
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C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-200' **Lext_change 21-Jul-2000
C;Accession: T45032
               hypothetical protein C24A3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 ::.C;Accession: T15584
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A; Introns: 47/2;
A; Note: Y39B6B.f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, F. tock, L.; Wilkinson-Sproat, J.; Wohldman, P. A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. A;Reference number: S43531; MUID:94150718
A;Accession: T45032
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Eraser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hiller, L.; Jier, M. B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, Nature 368, 32-38, 1994
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R; Favello,
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Best Local S
Matches 83
                                                                                                                                                                   325
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les 83; Conserv
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                                                                                                                                                                                                      YKPVVWFWILVGLAYFAAVLSMIGD
                                                                                                                                                                                                                                             V-VFASLLLFVFAIPAWVFSSIETDWSYLDAFYYCFVS!
                                                                                                                                                                                                                                                                                                                     PLTLALLSAIVARMREPSHKLRGLLNQRLGHLF - - - - -
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                                                                                                                                                                   YKIGATVYLMGGLCCMMLFLATLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIIGATVFKALEQPHEISQRTTIVIQKQTFISQHS-----CVNSTELDELIQQI-V 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REKCSKQ--KYSVISSKDDKNKEGDLNLDHLENYISIPI-L!VAILLSYITFGAVVLSMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -FSRIEYPLE-----KIEREAYLDYQNQWRDRLIQLDIDESEIDKLFLNIRE 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.0%;
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                                                                                                                                                                                                                                                                                                                                                        --GDQLGTIFGKGIAKVENTFIKWNVSQTKIRIISTI 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 273; DB 2;
Pred. No. 1.7e-14;
6; Mismatches 10C
                                                                                                                                                                                                      294
                                     20-Sep-1999 *:ext_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -IRIISTI i IIFGCVL-FVALPAIIFKHI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260/3;
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                                                                                                                                                                                                                                                                   SEGDYVAGGS-DIEYLDF 269
                                                                                                                                                                                                                                             GLGDFEPGDDPNQSFRGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 392
                                                                                                                                                                                                                                                                                                                     ----TVNHIQLIHVG
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                                      20-Sep-1999
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M.; Jo
D.
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submitted to the EMBL Data Library,

November

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hypothetical protein T01B4.1 - Caenorhabditis elegans (;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to C;Accession: T24265 R;Wilkinson, J.
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                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-522 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: T24265
                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, March 1996 A; Reference number: Z19866
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A;Introns: 21/1; 63/3; 131/1; 193/3; 206/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U40424; NID:g1065542; PID:g1065543; PIDN:AAA81455.1; CESP:C24AC;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-325 <FAV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: The sequence of C. elegans cosmid C24A3.
A;Reference number: Z18373
A;Accession: T15584
                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated
                                                                                                                                                                                                                                                             Map position: X
                                                                                                                                                                                                                                                                              Gene: CESP:T01B4.1
                                                                                                                                                                                                                                                                                                                 Cross-references: EMBL:270036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:T01B4.1: Experimental source: clone T01B4
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Best Local :
                                                                                                                                                                 Query Match
Best Local Similarity
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101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                      LILIILGYACLGGYMFQALEYDQQQLELEAEKRVRLSESSLLAVNLLEHLKQMNCGQSNE 100
                                                                                                         IFLVVVLYLIIGATVFKALEQPHE-----ISQRTTIVIQKQTFISQHSCVNSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS-----KKTKE 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TIIFILFGCVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKGIAKVEDTFIKWNVSQTKIRIIS-'----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STELDELIQQIVAAIN-------AGIIPLGNTSNQIS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LDELIQQIVAAINAGIIPLGNTS-NQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSFPISGLLLITVIWVIFCAVLETFLEEWDFGTSLYFTLISFTTIGFGDILP--SDYDFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AKGCKMLWRFFLK----STRVVSKDLSNKISEAADNIEEGTTAITPSAEKTENNDDDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HWTFLGSIFYCMTVYTTIGYGNIVPGTGWGRFATILYAFIGIPLTVLSLY----CLGSLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --ERDELIRRTVYKINQLQIKRQRRLMTAEEEEYNRTAKVLTTFQETLGIVPA--DMDKDI 112
----KRCLELITKTFIQRSDEERGEGWRWDFWNSVFFSATIFTTIGYGNLACKTNLGRI 155
                                                                                                                                                                                                                                       95/3; 142/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66;
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                                                                                                                                                Conservative
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                                                                                                                                                                                                                                       224/3; 290/1; 458/3
                                                                                                                                                                 12.7%;
23.1%;
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25.1%;
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; Pred. No. 2.9e-14;
53; 'Mismatches 88
                                                                                                                                              64;
                                                                                                                                              Score 266; DB 2; 1
Pred. No. 9e-14;
4; Mismatches 132;
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                                                                                                                                                                                 DB 2; Length 522;
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                                                                                                                                              Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 116;
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submitted to the EMBL Data Library, August A; Reference number: Z19377
A; Accession: T21118
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A;Molecule type: DNA
A;Residues: 1-452 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Swinburne, J.; Ainscough,
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Best Local
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276
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                                      256 DYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDELEVI 299
                                                                             216
                                                                                                                    203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 LKISGGRRSSSDASSVITEASDEDTRHFKVGRAILAEA! DERASNHGTQLNSCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238 ALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWII.--VGLAYFAAVLSMIGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 MLEVFFEVPEDDKEDTTFQLRWG-------LLV(VLFVVLCSFVVSFWENWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 FLTAFYFFFVSLSTIGFGDIVP------DHPRTACALFVLYFIGLALFAMVYAILQER 312
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                                                                                                                                                                                                                                                                                                                   36
                                                                                                                                                                                                                                     96 LATTENVAEINEHLRMFLRNISNLHISLDNYLIFNEPTQIVIKRWTFPSSVLFSFTILTT 155
                                                                                                                                                                                                                                                                            90 QHSCVNSTELDELIQQIVAAINAGIIPLGN-----TSNO\SHWDLGSSFFFAGTVITT 142
                                                                                                                                                                                                                                                                                                                                                        42 MKWKTVSTI-----FLVVVLYLIIGATVFKALE--- PHEISQRTTIVIQKQTFIS
                                                                                                                QTKIRIISTI----IFILFGCVLFVALPAIIFKHIEGW----SALDAIYFVVITLTTIGFG
                                                                                                                                                       IGYGNVTPHTQQCKVFLMIYGAFGIPLFLITIADLGRFSKTALMALVQKVSKRELKKQSD 215
                                                                                                                                                                                                                                                                                                                 MKFRNVLRIALGHLALYCFVVCYVFAGAWVFHQLEGENI FI IDKQREYAMNLKKDVIAK 95
  DIVP-----RRMDFLLPTL-IYITIGLWLTTALVEQLADVEKLV 313
                                                                             EHLLREIAEVSPYLDVLLVAGLFVVFIAIGSAVIPLWENQLTYFDSVYFSYMSLTTIGLG
                                                                                                                                                                                              IGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTLFGKGIAKVEDTFIKWNVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----W-LRVISKKTKEEVGEFRAHAAEWTANVT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31/1; 82/2; 101/3; 157/1; 197/1; 230/3;
                                                                                                                                                                                                                                                                                                                                                                                                 81;
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Pred. No. 1.6e
50; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 ,121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 452
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                             275
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hypothetical protein ZK1067.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T27681
R;Thomas, K.
                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein W06D12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26229
                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-444 <WIL>
A;Cross-references: EMBL:Z82073; PIDN:CAB04923.1; GSPDB:GN00023; CESP:W06D12.2
                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, November 1996
A;Reference number: Z20177
A;Accession: T26229
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A;Molecule type: DNA
A;Residues: 1-427 <WILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: T27681
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                                                                                                          A; Map position: 5
A; Introns: 70/3; 127/1;
                                                                                                                                                                                           A; Experimental source: clone W06D12
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A; Introns: 51/3;
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A;Experimental source: clone ZK1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                      Gene: CESP:W06D12.2
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  Matches
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Best Local
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                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --YMTISACVYTILEPMWSPLDSFYFCLVSLLTVGFGDLHPVGT-VEYM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSINFRAFKEGLKPTDFLVPQETSRWSMISAIFFTTTVLTSIGYGNLIPISTGGKIFCVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KFQ-----IMLELMGYSSKAFSFLRAPL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLFVALPAIIFKHIEG-WSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VA----AINAGIIPLG-NTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCII 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LCSIVFIFIGLILTTLAVDVSGSVGIAKMHSIGRGFDAMKMLNALRKKETVK---
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    81;
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    Conservative
                                                                                                            170/1; 197/3; 326/1; 405/3
                        11.8%;
20.8%;
    75;
Score 247; DB 2; 1
Pred. No. 2.5e-12;
5; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                          Length 444;
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    Indels
    108;
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354 GNVAEKYSENMEMGNKLLMRFMSNHQKKM 382
                                              334 VEIYDKFQRATSIKRKLSAELAGNHNQEL 362
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                                                                                                                                                                                                                                                                                                               GSIDKTPLMETSSTPPSPQNPNGTRPIPLLLVLIVLFFWMTQCVAY-----FAYFENW 250
                                                                                                                                                                                                                                                                                                                                                                                                                    GRICTMLYAMIGIPIVINILNDWGNMLFYFVDHFWQNIGRQW!OSLRQKLRRKVQSLEE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLIVYSFLGAGLFVLCEAENEKSLKHEDNMRVLRTSIAA . VFVQRLQNMYSGNGSSSEF
                                                                                                                                                   IGDWLRVISKKTKEEV-GEFRAHAAEWTANVTAE---
                                                                                                                                                                                                                                                     SALDAIYFVVITLTTIGFGDY-----VAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSM 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKIFCIIYALLGIPLFGFLLAGVGDQLGTI---FGKGIAKVEDTFIKWNVSQTKIR---- 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SETKLRRVLSEYDAAMGISI-----DSKMKTRWDIWGGLYYAGTIYTTIGYGDLAAETIW 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSTELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSF FAGTVITTIGEGNISPRTEG 154
                                                                                                  IQMQLEFIFNQIVQRIENDFKN----TLSVAAEESRKK3
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Search completed: August 28, 2001, 17:07:04 Job time: 473 sec

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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_vertebrate:*
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Q9NPC2
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Q17185
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                 O9hb59 homo sapien
O9h591 homo sapien
O9h591 homo sapien
O9jk62 mus musculu
O9z2t2 rattus norv
O9j158 cavia porce
O02821 oryctolagus
O9npc2 homo sapien
O9hbc8 homo sapien
O9hbc8 homo sapien
O96ru5 rattus norv
O9h592 homo sapien
O91104 rattus norv
O9h427 homo sapien
O9qx34 mus musculu
O17185 caenorhabdi
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Q9jis4 rattus norv
 Q9es08 rattus norv
Q9hb15 homo sapien
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Best Local :
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Q9JIS4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 275:17412-17419(2000).
EMBL; AF196965; AAF75132.1; -.
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MEDLINE=20298807; PubMed=10747911;

Bang H., Kim Y., Kim D.;

"TREK-2, a new member of the mechanosensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family.";
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                           LRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSIKRKLSAELA
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63.7%;
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Last annotation update)
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Pred. No. 6.2e-82;
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Sciurognathi;
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Query Match
Best Local Similarity
Matches 247; Conser
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01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Lesage F., Terrenoire C., Romey G., Lazdunsk, "Human TREK2, a 2P domain mechano-sensitive k regulations by polyunsaturated fatty acids, Gi, and Gq protein-coupled receptors.";
J. Biol. Chem. 275:28398-28405(2000).
EMBL; AF279890; AAG15191.1;
SEQUENCE 538 AA; 59764 MW; 8EA615B08D147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertei sta; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homo idae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=20435789; PubMed=10880510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2P DOMAIN POTASSIUM CHANNEL
                         350 LSAELAGNHNQELTPCRRTLSVNHLTNERDVLPP 383
                                                                                                        NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 170
                                                                                                                                                                                                                                                                                                                                           AAPDLLDPKSA-----AQNSKPRLSFSTKPTVLASF\\ SDT---TINVMKWKTVSTI
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                                                                                                                                                                                         GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRI : [[IFILFGCVLFVALPAIIF
                                                                                                                                                                                                                                                                                    FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISCHSCVNSTELDELIQQIVAAI 110
                                                                              SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKE:
                                                                                                                                                                                                                                                                         FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD
                                                                                                                                                                                                                                                                                                                            AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RF; 3:15QGGLQTVMKWKTVVAI 75
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  SME--
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RRRLGLDQRAHSLDMLSP
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Pred. No. 1.
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(TrEMBLrel. 16, (TrEMBLrel. 16,

Created)
Last sequence update)

PRELIMINARY;

PRT;

294

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RESULT
Q9JK62
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Best Local S
Matches 97
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001
DJ137F1.2 (N
                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                Q9JK62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL136087; CAC07336.1; ...
                                                                                                                                     Submitted
                                                                                                                                               "Mouse two P domain p
                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=129/SVJ; TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                     PRINTS; PR01333; 2POREKCHANEL.
                                          InterPro;
                                                                                                       TISSUE=KIDNEY;
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSTIFLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQI 106
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                               IPR001622; -. IPR003280; -.
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   502
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                                                                                                                                                                                                                                                                                              PRELIMINARY;
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 AA;
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Primates;
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) to the EMBL/GenBank/DDBJ
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Pred. No. 1.3e-28;
                                                                                                                                                                                                          Craniata; Vert
Sciurognathi;
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E4C7E7CC71B44D95 CRC64;
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InterPro; IPR003280; -.
Pfam; PP02034; TWIK Channel; 1.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01096; TWIK1CHANNEL.
Ionic Channel.
SEQUENCE 336 AA; 38228 MW; 5
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Q9ZZTZ
Q9ZZTZ;
Q1-MAY-1999 (TrEMBLrel. 10, Created)
Q1-MAY-1999 (TrEMBLrel. 10, Last sequence of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and localization of rTWIK, a putative votassiuntwo P domains.";
Submitted (SEP-1997) to the EMBL/GenBank/DDB1 3-tabases
EMBL, AF022819; AAD09336.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Verteb sta; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Maidae; Murinae; Rattus. NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gan L., Joiner
Kaczmarek L.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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85
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                   AINAGIIPLGNTSNQISHWDLGSSFEFAGTVITTIGEGN: A UECGKIECIIYALLGIP
                                                                                                    FLVV--VLYLIIGATVFKALEOPHEISORTTIVIQXQ\\ | SCVNSTELDELIQQIVA 108
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ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP
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                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000099;
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32.5%;
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InterPro; IPR001622; ...
InterPro; IPR003092; ...
InterPro; IPR003280; ...
InterPro; IPR003280; ...
Pfam; PF02034; TMIK_channel; 1.
PRINTS; PR01333; 2POREKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "TASK-3, a novel tandem proe domain acid-sensitive extracellular histidine as pH sensor.";
J. Biol. Chem. 275:16550-16557(2000).
EMBL: AF212827; AAF63706.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
POTASSIUM CHANNEL TASK3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rajan S., Wischmeyer E., Liu
Karschin A., Derst C.;
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  274
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                                                                                    RKPFYVAFSFMYILVGLTVIGAFLNLV--VLRFLTMNSDEERGEGEEGAALPGNPSSVVT
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yer E., Liu G.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.0%; Score 357.5; DB 11; 30.1%; Pred. No. 4.4e-18;
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Q9NPC2; Q9NPC2;
Q9NPC2;
Q9NPC2;
O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-CCT-2000 (TrEMBLrel. 16, Last annotation, pdate)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation, pdate)
2P DOMAIN POTASSIUM CHANNEL TASK-3 (POTASSIUM CHANNEL TASK3)
2P DOMAIN POTASSIUM CHANNEL KT3.2) (2P DOMAIN POTASSIUM CHANNEL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O02821 PRELIMINARY; PRT; 259 AA.

O02821;
O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-JUL-1997 (TrEMBLrel. 04, Last sequence u. 'u'e)
O1-MAR-2001 (TrEMBLrel. 16, Last annotation upodate)
DOUBLE PORE POTASSIUM CHANNEL RABKONKI (FRACHENI).
OTYCTOLAGUS CUNICULUS (RABbit).
Eukaryota; Metazoa; Chordata; Craniata; Verleb'ata: Euteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Cry'tolagus.
                                                                                                 Girard C., Lesage F., Ti
"Human Task-3, a novel 1
Submitted (JUN-2000) to
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                SEQUENCE FROM N.A. MEDLINE=20287530; PubMed=10747866; Rajan S., Wischmeyer E., Liu G.X.,
                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR003280; -.
PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                EQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTLLFLTAVVQRVTVHVTR--RPVLYFHVRWGFSKQVVAIVHAVLLGLITVSCFFFIPAA
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78; Conser
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259 ‡
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29311 MW; 5546A8BD278E7!
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Pred. No. 3.4e-18;
7; Mismatches 94
                   G.X.,
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Preisig-We;
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resell R.E., Murdock P.R., Randdall A.D., Rennie G.I., Gloger I.S.;
refloning, localisation and functional expression of a novel human,
reflected two pore domain potassium channel.";
L Brain Res. Mol. Brain Res. 82:74-83(2000).
reflected two pore domain potassium channel.";
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J. Biol. Chem. 275:16650-16657(2000).
    Q9HBC8;
01-MAR-2001
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InterPro; IPR003280; -.
Pfam; PF02034; TWIK_channel;
                                             о9нвс8
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Vega-Saenz de
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374 AA;
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PR01095; TASKCHANNEL.
    (TrEMBLrel.
                                             PRELIMINARY;
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    Created)
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Pred. No. 1.7e-17;
7; Mismatches 146;
                                           PRT;
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076795;
01-NOV-1998
01-NOV-1998
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
Vega-Saenz de Mies
Coetzee W., Rudy I
"KT3.2 and KT3.3"
                                                                                                                                                                                01-NOV-1998 (TREMBLIFE). 08, Created)
01-NOV-1998 (TREMBLEF). 08, Last sequence up
01-MAR-2001 (TREMBLEF). 16, Last annotation
PUTATIVE POTASSIUM CHANNEL SUBUNIT N2P38.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to TASK1.";
Submitted (APR-2000) to the
EMBL; AF257081; AAG33127.1;
                                                                                                 Wang Z.-W., Salkoff L.; Potassium channels in C. el Submitted (AUG-1998) to the EMBL; AF08352; AAG32863.1;
                                                                                                                                                                Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Last sequence ut 01-MAR-2001 (TrEMBLrel. 16, Last annotation TWO PORE POTASSIUM CHANNEL KT3.3.
                                   Ionic channel. SEQUENCE 329
                                                     Pfam; PF02034; TWIK_channel; PRINTS; PR01333; 2POREKCHANEL
                                                                      InterPro; IPR000099; InterPro; IPR001622; InterPro; IPR003280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ionic channel.
SEQUENCE 330
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Mammalia; Eutheria;
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                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            174
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91; Conservative
Similarity
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                                                                                                                                                                 Nematoda; Chromadorea; rinae; Caenorhabditis.
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Primates; Catarrhini; Ho
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                                    36992 MW;
16.4%;
33.7%;
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34
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                                                                                                                   . elegans
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                                                                                                                                                                                                                                                                                                          295
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Pred. No. 2.1e
42; Mismatches
                                                                                                           EMBL/GenBank/DD
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Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.H.P.,
                                                                                                                                                                                                                                           PRT;
                                    338A6D9A5774
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345;
No.
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                                                                                                                                                                                                                                                                                                                                                                -- NLVVAGLLACAATLAL
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                                    CRC54;
         Length
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                                                                                                                                                                           Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                               -WILVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
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RESULT
Q9H592
ID Q9
AC Q9
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PARESULT

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Best Local Similarity
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    Q9H592;
Q9H592;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
2P DOMAIN K+ CHANNEL TWIK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "TWIK-2, an inactivating 2P domain K+
J. Biol. Chem. 275:28722-28730(2000).
EMBL; AF:81304; AAG10508.1; -.
Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SPRAGUE-DAWLEY;
MEDLINE-20435832; PubMed-10887187;
Patel A.J., Maingret F., Magnone V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9ERU5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Honore E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                 195
                                                                                                                                                                                                                137
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                                                                                                                                                                   233 I-EGWSALDAIYFVVITLTTIGFGDYVAGGSDIE-YLDFYKPVVWFWILVGLAYFAAVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELIQQIVAAI--NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                              LLTASAQRLSLLLTH--APLSWLSLRWGWHPQRAARWHLVALLMVIVAIFFLIPAAVFAY
                                                                                                                                                                                                                                                     LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIFKH 232
                                                                                                                                                                                                                                                                                              LANASGPANASDPAWDFASALFFASTLYTTMGYGYTTPLTDAGKAFSIVFALLGVPITML 136
                                                                                                                                                                                                                                                                                                                                     LGNTSNQIS----HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGF 172
                                                                                                                                                                                                                                                                                                                                                                           YLALGALLVARLERPHEARLRAELGTLREQLLRHSPCVAAHALDAFVERVLAAGRLGRAV 76
                                                                                                                                                                                                                                                                                                                                                                                                                  YLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLV---FILFGLTVISAAMNLL--VLRFLTMNTEDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FCMLYALAGIPLGLIMFQSIGERMNTFAAKLL----RFİRRAAGKQPIVTSSDLIIFCT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILF
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                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34214 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.3%; Score 343; DB 11; Length 313; 32.2%; Pred. No. 4e-17; Indels tive 47; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A93629568785CD8F CRC64;
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                         229
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Q9JLD4
ID Q9JLD4
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Query Match
Best Local
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Ionic Channel.
NON_TER
Sports.
                                                                                                                                   "TASK-3, a New Member of the Tandem Pc
J. Biol. Chem. 275:9340-9347(2000).
EMBL; AF192366; AAF60229:1; -.
InterPro; IPR000099; -.
InterPro; IPR001622; -.
InterPro; IPR003092; -.
InterPro; IPR003380; -.
                                                                                                                                                                                                                                                                                                                                                                                                                              O9JLD4 PRELIMINARY;
O9JLD4;
O1-OCT-2000 (TrEMBLrel. 15,
O1-OCT-2000 (TrEMBLrel. 15,
O1-MAR-2001 (TrEMBLrel. 16,
                                                                  Pfam; PRO2034; TWIK channel; 1
PRINTS; PRO1333; 2POREKCHANEL.
PRINTS; PRO1095; TASKCHANNEL.
SEQUENCE 395 AA; 44365 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence upd re)
01-MAR-2001 (TrEMBLrel. 16, Last annotation of late)
DJ137F1.1 (NOVEL MEMBER OF THE POTASSIUM CHARRES SU
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-CEREBELLUM;
MEDLINE-20200422; pubMed-10734076;
KRIM Y., Bang H., Kim D.;
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                 POTASSIUM CHANNEL TASK3.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertur ata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DJ137F1.1
                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVQAYKNGASLLSNTTS-MGRWELVGSFFFSVSTITTIG) ...SPNTMAARLFCIFFALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GIPLNLVVL----NRLGHLMQQGVNHWASRLGGT----WQ-DPDKARWLAGSGALLSGLLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVAAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIG: %ALSPRTEGGKIFCIIYALL 165
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Similarity 36.4%;
79; Conservative 4'
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16.2%;
30.3%;
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 Score
Pred.
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Sciurognathi; Furidae;
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341; DB 11:
No. 7.5e-17;
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Best Local Similarity
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL118522; CAC14068.1; -.
SEQUENCE 330 AA; 36222 MW; 24F428721A1C7790 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TIEMBLIEL. 16, Created)
01-MAR-2001 (TIEMBLIEL. 16, Last sequence update)
01-MAR-2001 (TIEMBLIEL. 16, Last sequence update)
01-MAR-2001 (TIEMBLIEL. 16, Last annotation update)
DJ781B1.1 (A NOVEL PROTEIN SIMILAR TO THE ACID-SENSITIVE
CHANNEL PROTEIN TASK (KCNK3)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9H427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Lovell J.;
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                                                                 174 GAVAFSHFEGWTFFHAYYYCFITLTTIGFGDFVALQSG-EALQRKLPYVAFSFLYILLGL
                                                                                                                                                                                                             107 VAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLG 166
233 TVIGAFLNLVVLRFLVASADW 253
                                 283 AYFAAVLSMI------GDW 295
                                                                                                                                          118 IPLTLVTFQSLGERLNAVVRRLLLAAKCCLGLRWTCVSTE----NLVVAGLLACAATLAL
                                                                                                                                                              167 IPLFGFLLAGVGDQLGTIFGKGIAKVEDTF-IKWNVSQTKIRIISTIIFILFGCVLFVAL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 VPQSRKR 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 KPFYVAFSFMYILVGLTVIGAFLNLV--VLRFLTMNTDEDLLEGEVAQILAGNPRRVVVR 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 LDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEV--GEFRAHAAEWTANVTAE 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 ENMVTVGFFSCMGLVPW-AAAFSQCEDWSFFHAYYYCFITLTTIGFGDFVALQSKGALQR 215
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                                                                                                                                                                                                                                                                                  11 LVLCTLCYLLVGAAVFDALESEAE-SGRQRLLVQKRGALRRKFGFSAEDYRELERLALQ-
                                                                                                                                                                                                                                                                                                          50 IFLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQ---HSCVNSTELDELIQQI 106
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                                                                                     PAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF---WILVGL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKETRRR 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FCMFYAVLGIPLTLVMFQSLGERM------NTFVRYLLKRIKKCCGMRNTEVSM 156
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Search completed: August 28, 2001, 17:12:45 Job time: 414 sec

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Result
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Maximum Match 100%
Listing first 45.s
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1 MAAPDLLDPKSAAQNSKPRL.....LNGLTPHCAGEDIAVIENWK 411
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Copyright (c) 1993 - 2000 Compugen
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	nt of cancer,								ase;							S	Arabidopsis thalia	idopsis	S	Arabidopsis thalia	Arabidopsis thalia	Human potassium ch	Amino acid sequenc	Caenorhabditis ele	Amino acid sequenc	Amino acid sequenc F22b7.7 potassium	2	U	<u>"</u> "	Human potassium ch Human hTREK-1 prot	Protein encoded by	9	Human potassium ch Human signal pepti		TWIK-	Human protein clon Amino acid sequenc

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25-FEB-1998;
07-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY34133 standard; Protein;
                                                                                                               22-FEB-1999;
                                                                                                                                                            02-SEP-1999
                                                                                                                                                                                                       W09943696-AI
                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                 Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome; cardiovascular disorder; CNS disorder; renal disorder.
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98US-0076687.
98US-0095836.
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0; Mismatches
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1.4e-217;
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This sequence represents the human K+Hnov59 go ssium channel.

CK HHnov proteins have a high degree of homology to known potassium channels and may be alpha subunits, which form the functional channel, or accessory subunits that act to modulate the channel activity. K+Hnov59 is a 4 transmembrane domain, 2 pore domain potassium channel. The gene coil calisation using primers Azzl1939 and Azzl1940, K+Hnov DNAs covere isolated by extension of expressed sequence tags (ESTs) which were concluded by extension of expressed sequence tags (ESTs) which were concluded but not identical to known human potassium channels. Potential polymorphisms detected as sequence variants between multiple coil types and biochemical pathways. Defective potassium channels are coil types and biochemical pathways. Defective potassium channels are cardiac arrhythmia (long QT syndrome); epilopsy: and Bartter's syndrome. Coil tis likely that abnormal potassium channels or also implicated in certain renal, cardiovascular and central nervous system (CNS) coidentifying homologous or related proteins and the DNA sequences encoding them. They may be used to produce compositions that modulate the coinchemical pathways associated with it. They may also be used for the treatment of diseases associated with abnormal potassium channels for the treatment of diseases associated with abnormal potassium channels.
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411
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Вb Ş DЬ δÃ В Qγ В Qy 밁 Qγ 밁 Qy Query Match Best Local Matches 181 361 301 301 241 241 121 121 181 61 61 GAAVFKALEQPQEISQRTTIVIOKQTFIAOHACVNSTELA COIVAAINAGIIPLGNS 396; Similarity Conservative 97.8%; Score 2044; DB 20; 96.4%; Pred. No. 3.1e-213; Mismatches D. ATSVKRKLSAELAGNHNQ 3 Length 411; Indels 0 Gaps 180 120 360 180 120 60 60 300 300 240 240

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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-OCT-1998;
27-JAN-1998;
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                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                              stroke, and head trauma and neurological disorders including migraine.
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3;
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DB; AAZ00039.
                      maapdlldpksaaqnskpr1sfstkptvlasrvesdttinvmkwktvstiflvvvlylii
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 AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS
                                                                                             SNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  pore potassium channel used for, e.g. treary, cardiovascular and inflammatory diseases
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98EP-0300570.
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96.4%;
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Query Match Best Local Matches 39

Local Similarity

97.8%; 96.4%;

Score 2044; DP Pred. No. 3.1e-1; Mismatches

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                                 The present sequence is human TREK1 (h-TREY). h-TREK1 is a member of the 2P domain potassium channel family of prote. hich play a part in the control of resting membrane potential. Modular on of these channels will therefore affect neuronal excitability, thereby leading to a modulation of neurotransmitter release and activity of neuronal networks. Such modulation therefore may be useful for the treatment of certain neurological conditions such as epilepsy, sic exclated disorders, cognitive dysfunction, attention deficit diso war, addiction, anxiety/phobia, Parkinson's and Huntington's curea, cerebral palsy,
                                                                                                                                                                                                                                                                   WPI;
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neurological disorder; sleep-related disorder;
attention deficit disorder; addiction; anxiety
                                                                                                                                                                                                  Use of human TREK1 polypeptide, polynucleot modulators of h-TREK1 polypeptides for treadisorders, addiction and dyskinesias include
                                                                                                                                                                Claim 7; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erectile dysfunction; alopecia
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Sequence
                                                                                                                                                                                         Huntington's
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DB; AAC90412.
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The present sequence represents a mechanically sensitive potassium channel protein designated TREK-1. The protein is activated by polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nervous systems in humans and animals, e.g. epilepsy, cardiovascular disease (arrhythmia), neurodegeneration (particularly where associated with
                                                                                      Claim 3;
                                                                                                           New mechanically sensitive potassium channel, used specific modulators, potential therapeutic agents i system disorders .
                                                                                                                                                                                    Honore
                                                                                                                                                                                                                            05-MAR-1998;
                                                                                                                                                                                                                                                                                           W09945108-A2
                                                                                                                                                                                                                                                                                                                Mus
                                                                                                                                                                                                                                                                                                                                     muscular
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                                                                                                                                                                                                       (CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                              neurodegeneration;
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                                                                                                                                                                                                                                                                                                                                                        polyunsaturated fatty acid; arachidonic acid; riluzole; huservous system disease; epilepsy; cardiovascular disease;
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                                                                                                                                                    AAZ10607
                                                                                    Page 23-25; 40pp; French.
                                                                                                                                                                                                                                                                                                                                     disease.
                                                                                                                                                                                   Fink M,
                                                                                                                                                                                                                                                                                                                                                                              sensitive potassium channel
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                                                                                                                                                                                                                            98FR-0002725
                                                                                                                                                                                                                                                 99WO-FR00404
                                                                                                                                                                                                                                                                                                                                               ischemia;
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                                                                                                                                                                                  Lazdunski M,
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                                                                                                                                                                                                                                                                                                                                              anoxia; hormone secretion abnormality;
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                                                                                                                                                                                  Lesage
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                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                  Duprat
                                                                                                                                                                                                                                                                                                                                                                  riluzole; heart disease;
                                                                                                                    d to
                                                                                                                                                                                                                                                                                                                                                                             TREK-1;
                                                                                                                    heart and nervous
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Best Local S
Matches 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ischemia or anoxia), abnormalities of hormon to cretion and m disease. The protein itself may be used to the content and mathbodies specific for the protein are use the detect it in also as therapeutic inhibitors or activators.
        N-PSDB; AAA27105
                WPI; 2000-365583/31
                                Chapman CG,
                                                                  03-NOV-1998;
07-OCT-1999;
                                                                                           03-NOV-1999;
                                                                                                                                                              2P domain potassium channel; neurodegenerat psychiatric disorder; neurological disorder:
                                                                                                                                                                               Human; h-TRAAK; potassium channel polypeptic;
                                                                                                                                                                                                Human h-TRAAK
                                                                                                                                                                                                                   04-AUG-2000
                                                                                                                                                                                                                                                     AAY94425 standard;
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                                                                                                                             WO200026253-A1
                                                                                                                                              Homo sapiens
                                                 (SMIK)
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367; Conser
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                                Duckworth
                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                polypeptide
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                                                                 98GB-0024048
99GB-0023668
                                                                                           99WO-GB03634
                                                  BEECHAM
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99.7%;
                                 DM:
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Pred. No. 9
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                                                                                                                                                                      stroke
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Best Local S
Matches 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK polynucleotides from human tissue samples. h-TRAAK polypeptides have homology to the 2P domain potassium channel family of polypeptides. The h-TRAAK polypeptides and polynucleotides may be used in diagnostic assays for conditions related to h-TRAAK polypeptides. The h-TRAAK polypeptides and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and polynucleotides may also be useful for treatment and prevention (e.g. as vaccines) of certain diseases, such as pain, psychiatric disorders including depression and schizophrenia, neurodegenerative disease including Alzheimer's, stroke and head trauma and neurological disorders including migraine and epilepsy. The present sequence is human h-TRAAK protein #1.
                              03-NOV-1998;
07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                AAY94426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated h-TRAAK polypeptides belonging to the potass: family of polypeptides, useful for the diagnosis and treatment h-TRAAK related disorders, e.g. depression and schizophrenia
                                                                        03-NOV-1999;
                                                                                                                              WO200026253-A1
                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                            Human h-TRAAK polypeptide #2
                                                                                                                                                                                                                                                                         04 - AUG - 2000
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 (SMIK ) SMITHKLINE BEECHAM PLC
                                                                                                                                                                                     psychiatric
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nes 145; Conserv
                                                                                                                                                                                 man; h-TRAAK; potassium channel polypeptide;
domain potassium channel; neurodegenerative disease;
ychiatric disorder; neurological disorder; Gene theraj
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                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                      (first entry)
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                            98GB-0024048.
99GB-0023668.
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                                                                        99WO-GB03634
                                                                                                                                                                                                                                                                                                                              Protein; 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.1%; Score 797; DB 21; 51.1%; Pred. No. 7.5e-78; tive 60; Mismatches 77;
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                                                        muscular
                                                                                         Mechanically sensitive potassium channel protein; TRAAK; polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;
                                                                                                                            A mechanically sensitive potassium channel protein TRAAK
                                                                                                                                                                              AAY30647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional genomics was used to identify h-Trahh-TRAAK polynucleotides from human tissue samp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated h-TRAAK polypeptides belonging family of polypeptides, useful for the diagnes h-TRAAK related disorders, e.g. depression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chapman CG,
                                  Mus sp
                                                          neurodegeneration;
muscular disease.
                                                                               nervous system disease; epilepsy; cardiovascular disease;
                                                                                                                                                      18-NOV-1999
                                                                                                                                                                                                     AAY30647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epilepsy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pages 21 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is human h-TKAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                    Protein;
                                                                     ischemia;
                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.1%;
51.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
                                                                                                                                                                                                    398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 797; DB 21;
Pred. No. 7.5e-78;
iO; Mismatches 77;
                                                                     anoxia;
                                                                                                                                                                                                     ĀΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                     hormone
                                                                     secretion abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'cluding depression and ng Alzheimer's, stroke and ding migraine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : "izophrenia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein #2.
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;. h-TRAAK
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                                                                                                                                                                                                                                                              284
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of
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WO9945108-A2

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RESULT
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XX AAY2
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DT 12-C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a mechanically sensitive potassium channel protein designated TRAAK. The protein is activated by polyunsaturated fatty acids, particularly arachidonic acid, and by riluzole. The protein is used to screen for specific modulators which are useful for treating or preventing diseases of the heart and nervous systems in humans and animals, e.g. epilepsy, cardiovascular disease (arrhythmia), neurodegeneration (particularly where associated with ischemia or anoxia), abnormalities of hormone secretion and muscular disease. The protein itself may be used to treat these diseases. Antibodies specific for the protein are used to detect it in tissues, also as the protein are used to detect it in tissues.
  Homo
                                                                                                                             AAY28498
                             chromosome 1q32
                                          partial h-TREK1;
                                                                   Partial h-TREK1 polypeptide
                                                                                                  12-OCT-1999
                                                                                                                                                         AAY28498 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CNRS ) CNRS CENT NAT RECH SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 49.8 es 142; Conservative
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  sapiens
                                                                                                                                                                                                                                                                                                CVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI 278
                                                                                                                                                                                                                                                                                                                                                                                                                        LIQQIVAAINAGIIP----LGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                               mrsttllallalvllylvsgalvfqaleqpheqqaqkkmdhgrdqflrdhpcvsqksled 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as therapeutic inhibitors or activators.
                                                                                                                                                                                                                                                                                                                                                                  CIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFG
                                                                                                                                                                                                                                                                                                                                                                                            fikllvealggganpetswtnssnhssawnlgsafffsgtiittigygnivlhtdagrlf 120
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                                          two
                                                                                                                                                         Protein; 107
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49.8%;
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                                        pore potassium channel;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 770.5; DB:
Pred. No. 5.8e-75,
6; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                                                                                         Lesage F,
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Best Local S
Matches 107
Human; TWIK-3; TWIK-4; TWIK-2; central nerve, a system disorder; dementia; Trandem of p domains in a Weak Inward rectif; ng K4 channel; epilepsy; Alzheimer's disease; Parkinson's disease; mutiple sclerosis; depression; amyotrophic lateral sclerosis; progressive supranuclear palsy; mania; Creutzfeldt-Jacob disease; psychiatric disorfer; schizophrenic disorder; Korsakoff's psychosis; anxiety disorder; ph; C lisorder; amnesia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiovascular, and inflammatory diseases, paincluding depression and schizophrenia, neuronincluding Alzheimer's, stroke, and head traumalumcluding Alzheimer's,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide AAZ00041. AAZ00039 and ĀĀY28490 re complete h-TREK1 polynucleotide and polypeptide sequences. h-10001 is a two pore potassium channel, and the gene maps to human romosome 1932, between the markers D1S237 and WIS105. The polynucleo' is sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptide. The methods of diagnosis may be used in the treatment of diseases including cancer, pulmonary, may be used in the treatment of diseases including cancer, pulmonary,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is a partial h-TREK1 polypeptive polynucleotide AAZ00041. AAZ00039 and AAX28496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 25; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New two pore potassium channel used for, e.g. rea pulmonary, cardiovascular and inflammatory distributes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-OCT-1998;
27-JAN-1998;
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98EP-0300570
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; Pred. No. 5.7
; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease), psychiatric disorders (e.g. depression, schizophrenic disorders, Korsakoff's psychosis, mania, anxiety disorders or phobic disorders), learning or memory disorders (e.g. amnesia or age-related memory loss), neurological disorders (e.g. migraine), obesity, and cardiac disorders. The nucleic acids, proteins, protein homologues and antibodies against them may be further used in screening assays, predictive medicine. The nucleic acids can be inserted into vectors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New tandem of P domains in a weak inward rectifying potassium channel proteins and genes for e.g. developing therapeutic agents for potassium channel associated disorders, e.g. central nervous system, psychiatric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 148pp; English
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N-PSDB; AAA37770, AAA37771.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSA 352
                                                                                                                                                                                                                                                                LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHI
                                                                                                                                                                                                                                                                                                                                                                            IIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFL 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents the human TWIK-2 protein of the invention.
                                                                                                                                                                                                                                                                                                                               vaitgnqt--fnnwnwpnamifaatvittigygnvapktpagrlfcvfyglfgvpl----c
                                                          egwnyieglyysfitistigfgdfvagvnpsanyhalyryfvelwiylglaw----lslf
                                                                                                                                EGWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAYFAAVLSMI
                                                                                                                                                                                                  ltwi-salgkffggrakrlgqfltkrgvslrkaqitctvifivwgvlvhlvippfvfmvt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          as gene therapy vectors, to express TWIK protein, to detect TWIK modulate TWIK activity, and screen for drugs or compounds that ate TWIK activity. Host cells may be used to produce non-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  animals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 420; DB 21;
Pred. No. 9.4e-37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120;
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The present sequence is that of human TASK2 (TWIK-related acid-sensitive potassium channel 2), a novel member of the 2p domain potassium channel family that also includes TW-K-1 (see AAY79673) and TASK1 (see AAY79674). TASK2 is a unique potas ium transport channel that is regulated by external pH, and is predc inantly expressed in kidney and epithelial tissues. The invention clates to: identification of the native renal channel with the properties of TASK2; identification of potent pharmacology that specifically modulates the activity of the TASK2 subunit in viv: ind the generation of mice in which the TASK2 subunit in viv: ind the generation of mice in which the TASK2 gene has been in viv: ned the invention also relates to diagnostic tests and therapeutic methods to: detect
                                                                                                                                                                                                                                                                                                   New nucleic acid encoding a non-inactivating potassium transport channel, designated TASK, of hypertension or dysfunctions of the kidne,
                                                                                                                                                                                                                                                              Claim 16; Fig 14a; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-1998;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TASK2; TWIK-related acid-sensitive K+ chann: 2 human;
                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-376487/32
                                                                                                                                                                                                                                                                                                                                                                                                                                            Duprat F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1999;
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99US-0436265
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190..2:
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Best Local :
24-JUL-1998;
07-AUG-1998;
25-AUG-1998;
09-SEP-1998;
29-SEP-1998;
                                                                                                                                                                                                                                                                                                                      Human protein; hydrophobic domain; nutritional source; haematopoiesis; cytokine production; cell proliferation; cell differentiation; immune deficiency; infectious disease; autoimmune disorder; asthma; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; periodontal disease; asthmator disorder; osteoporosis; osteoparthritis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pancreas and/or liver dysfunctions that may arise from mutations the TASK2 gene; protect against tissue rejection in kidney, pancr and liver transplants; and identify potential drugs capable of modulating TASK2 activity.
                                                                                                                                                                                                                                                                     nervous system disorder; Alzheimer's disease; Parkinson's disease
Huntington's disease; liver fibrosis; lung fibrosis; reperfusion
systemic cytokine damage; tissue differentiation; contraceptive;
                                                                                                                                                                WO200005367-A2
                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein clone HP10538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY94875 standard; Protein; 499
                                                                                                  22-JUL-1999;
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                             coagulation disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e-ssphs----rkalqvkgstaskdvnifsflskkeety
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELAGNHNQELTPCRRTLSVNHLTSEREV--LPPLLKAESIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                egwnyleglyysfitistigfgdfvagvnpsanyhalyryfvelwiylglaw----lslf
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ltwi-salgkffggrakrlgqfltkrgvslrkaqitctvifivwgvlvhlvippfvfmvt 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHI 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaitgnqt--fnnwnwpnamifaatvittigygnvapktpagrlfcvfyglfgvpl---c
                                                                                                                                                                                                                                            shock; sepsis;
                                                                                                                                                                                                                               therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
 98JP-0208820.
98JP-0224105.
98JP-0238116.
98JP-0254736.
98JP-0275505.
                                                                                                99WO-JP03929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypertension and diseases associated with kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -kvsmf----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.1%;
                                                                                                                                                                                                                                                             myocardial infarction;
                                                                                                                                                                                                                                            ischaemia; reperfusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
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Pred. No. 9.
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.4e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120;
                                                                                                                                                                                                                                            injury; arthritis;
                                                                                                                                                                                                                                                             inflammatory condition;
                                                                                                                                                                                                                                                                                                            Parkinson's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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of
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                                                                                                                                                                                                                                                                            stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in
                                                                                                                                                                                                                                                                                          injury;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other cytokines in certain cell populations. Protein also exhibits commune stimulating or immune deficiencies and is riders, and to treat the creatment of various immune deficiencies and is riders, and to treat confections. The protein is also used for treat of unitable sclerosis, systemic lupus ery hematosus, and rheumatoid conditions such as asthma, and in immune suppression after organ conditions such as asthma, and in immune suppression after organ conditions such as asthma, and in immune suppression after organ conditions such as asthma, and in immune suppression after organ conditions such as asthma, and in immune suppression after organ crassplantation. The protein is useful in regulation of haematopoiesis and consequently in the treatment of myeloid o lymphoid cell conditions the protein is also used in the reatment of osteoporosis or osteoarrhritis and in the treatment of production of the conditions consisted tooth repair processes. The protein is used in the reatment of seteoporosis constead in the protein is used in the reatment of nervous system disorders such as Alzheimer's disease, arkinson's disease, and contraction and conditions resulting from system crous regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from system crotokine damage. They are also used for promoting or inhibiting tissue inferentiation. They are conditions resulting from coagulation activities end prevention of conditions resulting from coagulation activities end prevention of inhibitors or agonists of receptor/liqand interactions. They are used to
                                                                                                                                                                                                                                                                            Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human proteins having hydrophobic domains useful for treating osteoporosis, Alzheimer's disease, Parkinson's disease, asthma, multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibitors or agonists of receptor/ligand interactions. They are used treat inflammatory conditions such as septic shock, sepsis, ischaemia reperfusion injury, arthritis, and nephritis. They can be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nutritional sources or supplements. The proto, exhibits cy proliferation, cell differentiation activities and induces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                            EGWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAYFAAVLSMI
                                                                                                                                     LAGYGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHI
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                                                                                                                                                                                                                                                                                                                                                                                       Score 420; DB 21: Pred. No. 9.4e-37
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293

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                                                                                                                                                                                                                                                                                                               New tandem pore domain weak inward rectifying potassium ion (TWIK) channel nucleic acids and proteins, useful in assays for identifying candidate compounds which are potential pesticides or therapeutics -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                Claim 5; Page 87-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Francis-Lang HL,
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274..2
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Jeschke P;
                      for screening
                                         invertebrate
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TWIK3, TWTV'
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                                       New tandem of P domains in a weak inward rect, ying proteins and genes for e.g. developing theraphatic channel associated disorders, e.g. central nervous disorders
                                                                                                                                                                                                                                                                                                                  Rorsakoff's psychosis; anxiety disorder; phobic disorder; amnesia; learning disorder; memory disorder; age-related memory loss; obesity; neurological disorder; pardiac disorder; age-related memory loss; obesity;
                                                                                                WPI; 2000-572183/53.
N-PSDB; AAA37766, AF
                                                                                                                                                                                                                                                                                                                                                      amyotrophic lateral sclerosis; progressive sur unuclear palsy;
Creutzfeldt-Jacob disease; psychiatric disord. : schizophrenic
                                                                                                                                                                                                                                                                                                                                                                           Human; TWIK-3; TWIK-4; TWIK-2; central nervous system disorder; dementia; Tandem of P domains in a Weak Inward rectifying K+ channel; epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prognosis
                                                                                                                                       Curtis
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                                                                                                                                                                                                                                                                                                                 neurological disorder; cardiac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mflcsgaavfsyfeapeeralrvklgtavqkflvsnpnvtdadleeliveivrannrgvs 114
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                                                                                                                                       RAJ;
                                                                                                                                                             MILLENNIUM PHARM INC
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                                                e.g. central nervous system,
                                                                                                                                                                                                                                                                                                                 disorder;
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                                               potassium channel
agents for potassium
system, psychiatric
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Claim 8; Fig

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148pp; English

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Best Local (
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(CNRS ) CNRS CENT NAT RECH SCI
                                     08-FEB-1996;
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                                                                         08-FEB-1996;
                                                                                                                 14-AUG-1997.
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                      TWIK-1 potassium channel protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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| ::| |:|||| : | ||||:|:|
ppllfshmegwsytegfyfafitlstvgfgdyvigmnpsqryplwyknmvslwilfgmaw 255
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                                                                                                                                                                                                                            potassium channel; screening; diagnosis; transgenic animal;
of P domains in a Weak Inward rectifying K+; antibody.
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                                     96FR-0001565
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Pred. No. 2e-33;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for modulating activity of TWIK-1 type channe's may also be useful therapeutically, e.g. for control of epileps, arrhythmia, vascular disease, neurodegeneration (particularly of ischaemic or anoxic origin), endocrine or muscular disorders. The CDMA and the vectors can also be used to create transgenic animals (especially knock-out animals) for use as models of TWIK-1 related diseases. Analysis of the sequence of the TWIK-1 gene may be used for pre-natal diagnosis of disease. Antibodies can be used to detect TWIK-1 channels and for inhibiting or activating the channels in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            channels consisting of 4 transmembrane segme: 3 and two P domains, being only weakly rectifying. The CDNA, vect. 3, the cells express TWIK-1 type channels and the protein are use to compensate for deficiency of potassium channels in varias tissues. Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a protein commising a potassium channel with the properties of a TWIK (Tandem of P downins in a Weak Inward rectlifying K+) 1 channel. This is the first "ber of a new family of channels consisting of 4 transmembrane segme" and two P domains, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid encoding new potassium channel \text{des} ignated TWIK-1 -useful for treating channel deficiency diseases, screening for active agents and for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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Lesage F,
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                                    FAAVLSMIGDWLRVISK----KTKEEVGEFRAHAAE 316
                                                                                                                                                                 LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRI; LI
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DB; AAT64960.
                                                                                                                                            ftllfltavvqritvhvtr--rpvlyfhirwgfskqvvai nvllgfvtvscfffi--p
mlvvletfce-lhelkkfrkmfyvkkdkdedqvhiie
                                                                        aavfsvleddwnflesfyfcfislstiglgdyvpgegynqkirelykigitcylllglia
                                                                                                          AVIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GSDI': LDFYKPVVWFWILVGLAY
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                                                                                                                                                                                                                                                                                                                                                               18.0%; Score 376.5; LB 1 32.5%; Pred. No. 2.8e-32; tive 62; Mismatches 10H
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to compensate
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Search completed: August 28, 2001, 17:05:47 Job time: 1892 sec

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Scoring table:

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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-332-312-4
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Best Local Similarity
Matches 410; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 6
LENGTH: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6242217el Compound
FILE REFERENCE: GP30031
CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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US-08-953-823A-5

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US-08-637-823B-3

US-08-466-886-1

US-08-466-886-1

US-08-469-461-4

US-08-637-823B-3
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Pred. No. 2.2e
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RESULT 3
US-09-236-080-4
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US-09-236-080-2
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Best Local Similarity 96.4
                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4 LENGTH: 107
                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                              Sequence 4, Application US/09236080 Patent No. 6242217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 2 LENGTH: 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09236080 Patent No. 6242217
                                                                                          CURRENT APPLICATION NUMBER: US/09/236,080 CURRENT FILING DATE: 1999-01-25 NUMBER OF SEQ ID NOS: 6
                                                                                                                                                APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: No. 6:
FILE REFERENCE: GP30031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/236,080 CURRENT FILING DATE: 1999-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
TITLE OF INVENTION: NO. 6242217el Compounds
FILE REFERENCE: GP30031 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
ORGANISM: Homo
                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                             ELTPCRRTLSVNHLITSEREVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQ 360
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sapiens
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                                                                                                                                                                     6242217el Compounds
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                                                                                                        Query Match
Best Local (
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Best Local Similarity
                                                                                           Matches
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                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 15-NOV-1996
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Weiser, Gerard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 DQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVAL 225
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                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15 CLASSIFICATION:
                                25
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 19102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 230 South | CITY: Philadelphia
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                                                           51 FLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTF
                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version
                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: WEISER & ASSOCIATES STREET: 230 South Fifteenth Street,
                                FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRF
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                                                                                                          Similarity
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                                                                                                                                                                                                                                    336 amino acids
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Guillemare, Eric
                                                                                           Conservative
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Lazdunki, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barhanin, Jacques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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THEIR CLONING AND THEIR SE ESPECIALLY FOR THE SCREENING
OF DRUGS
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                                                                                                        18.0%; Score 376.5; 32.5%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                         19,763
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                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pausch, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                166 GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVS-----QTKIRIISTIIFILF-G
                                                                                                              106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGLIA
129 GIPVNGILFAG----LGEYFGRTFEAIYRRYKKYKMSTDMHYVPPQLGLITTVVIALIPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260 MLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 FAAYLSMIGDWLRVISK-----KTKEEVGEFRAHAAE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 AVIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 FTLLELTAVVQRITVHVTR--RPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFI--P
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                                                                      69 ISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNISPTTFAGRMIMIAYSVI 128
                                                                                                                                                                            50 IFLVVVLYLIIGAAVFKALEQPQE----ISQRTTIVIQKQTFIAQHACVNSTELDELIQQ 105
                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: P-38,711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Harrington, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                      CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                          IVAAINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
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                                                                                                                                            LLIFYISYLMFGAAIYYHIEHGEEKISRAEQRKAQIAINEYLLEELGDKNTTTQDEILQR
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Pausch, Mark H.
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                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                     14.3%; Score 299.5;
25.7%; Pred. No. 6.
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                                                                                                                                                                                                                    6.1e-23;
ches 151;
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                                                                                                                                                                                                                                                          Length 618;
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                                                                    Matches
                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                            TELEFAX: 201-831-3305 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
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APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Functional Expression
TITLE OF INVENTION: Melanagaster Putative
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 201-831-3246
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                              120 SSNQVSH------WDLGSSFFFAGTVITTIGFGNISPR1 GGKIFCIIYALLGIPLFGFL 173
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15 TSNEVKKNAATETWTFSSSIFFAVTVVTTIGYGNPVPVTNIGKTWCILFSLLGIPL---T
                                                                                                                                                                                                            TYPE:
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                                                                                                                                                                                                                                                                                                                                             NAME: Harrington, James
REGISTRATION NUMBER: P-
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                Score 219; DB L; L
Pred. No. 7.4e-15;
Pred. No. 7.7e-15;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: INVENTION: INVENTION: ITITLE OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 988
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                   11 SAAQNSK-PRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLIIGAAVFKALE 69
                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 15-NOV-1996
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                                                                   SMEENSKIQMLSATSKDKKVATDRSLLNKYHLGPLALHTGLVLSCVTYALGGAYLFLSIE 63
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230 South Fifteenth Street,
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FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
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----REFQDLKQQFMGNITSGIENSEQSIEIYTKKLI 108
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                                                                                                                                       Score 184.5; DB 3
Pred. No. 3.9e-11;
4; Mismatches 114
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US-08-749-816-3
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                                                         Query Match
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                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                    NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19 REFERENCE/DOCKET NUMBER:
 52 LVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIACHACVNSTELDELIQQIVAAIN 111
                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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                                            Local Similarity
                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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230 South Fifteenth Street,
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Barhanin, Jacqu
                              Conservative
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PC-DOS/MS-DOS
                                            23.78;
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THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
OF DRUGS
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                                            Score 160.5; DB 3
Pred. No. 1.1e-08;
                              Mismatches
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                                                          DB 3;
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                              Indels
                                                          Length 347;
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                             Gaps
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SEQ ID NO 2
LENGTH: 676
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/874,655
EARLIER FILING DATE: 1997-06-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 80
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APPLICANT: Keating, Mark T.
TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KYLQT1 WHICH
TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
FILE REFERENCE: 2323-128
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                    EEVGE---
                                                                                                                   VFIHRQELITTLYIGFLGLIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVVTVTTIG
                                                                                                                                       IFI---LFGCVLFVALPAVIFK----------HIEGWSALDAIYFVVITLTTIG
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                                                                                                                                                                                                                                                                                             NAG---IIPL---GNSSNQVSHWD-------LGSSFFFAGTVITTIGFGNISPRTE 153
                                                                                                                                                                                                                                                                                                                                    FLIVLVCLIF -- SVLSTIEQYAALATGTLFWM-----
                                                                                                                                                                                                                                                                                                                                                                 FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                     AAPDL----LDPKSAAQNSKPRLS-FSSKPTVLASRVESDSAINVMK----WKTV---STI 50
                                                                                  FGDYVAGGSDIEYLDFYKPVVWF-----WILVGLAYFAAVLSMIGDW--LRVISKKTK
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 -FRAHAAE-----
                                                 ---POTWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQ
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-WTANVTAEFKETRRRLSVEIYDKFQRATSV
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LENGTH: 581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Splawski, Igor
APPLICANT: Keating, Mark T.
TITLE OF INVENTION: A HONOZYGOUS MUTATION IN K.
TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
FILE REFERENCE: 2323-128
CURRENT APPLICATION NUMBER: US/09/135,021A
CURRENT FILING DATE: 1998-08-17
EARLIER APPLICATION NUMBER: 08/874,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/094,477
EARLIER FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.0
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                                  337 YDKFQRATSVKRKLSAELAGNHNQELTPCRRTLSVNHL1
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                                                                                                                                                          FVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF------
                                                                                                                                                                                                                          QTKIRIISTIIFI---LFGCVLFVALPAVIFK------
                                                                                                                                                                                                                                                                                                                                 ----EIVLVVFFGTEXVVRLMSAGCRSKYVGLMGRLRF
SPKPKKSVVVKKK---KFKLDKDNGVTPGEKMLTVPHIT
                                                                                                                                    WGVVTVTTIGYGDKV-------PQTWVGKTIASCFSVFAISFFALPAGILGSGF
                                                                                                                                                                                                       ----RLLGSVVFIHRQELITTLYIGFLGLIFSSYFVYLA .
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                                                                                                                                                                                                                                                                                                           GFGNISPRTEGGKIFCIIYALLGIPLFGFL-LAGVGDQL: FGKGIAKVEDTFIKWNVS 202
                                                                                                      -LRVISKKTKEEVGE-----FRAHAAE----
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                                                                    ALKVQQKQRQKHFNRQIPAAASLIQTAWRCYAAENPDSS:::KIYIR---KAPRSHTLLSP
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                 :|. .EATAb 383
. ---PP 353
                                                                                             " TANY "AEFKETRRRLSVEI
                                                                                                                                                                      ... LVGLAYFAAVLSMIGDW-
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RESULT 11 US-08-677-734A-11

Sequence 11, Application US/08677734A Patent No. 5871919 GENERAL INFORMATION:

APPLICANT:
APPLICANT:

Brant, Steven R. Yun, Chris C.H.

Donowitz, Mark

US-08-677-734A-12

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Query Match 4.9%; Score 101.5; DB 2; Best Local Similarity 19.0%; Pred. No. 0.072; Matches 71; Conservative 59; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 408-4000
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TITLE OF INVENTION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
333
                                       316 EWTANVTAEFKET 328
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                                                                                                                                                                                                                                                                                                       197
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                                                                                                                                                                                                                                                                                                                                                                                     146 GNISPRTEGGKIFCIIYALL
                                                                                  273 TRFTKHVRIIEPGFVFVISYLSYLTSEMLSLSAILAITFCGICCQKYVKANISEQSATTV 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/677,734A FILING DATE: 10-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
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RYTMKMLASGAET 345
                                                                                                                                                                                                                                                                                                   IKWNVSQTKIRIISTIIFILFGCVLFVALPA------VIFKHIEGWSALD--- 240
                                                                                                                            GDW---LRVI----
                                                                                                                                                                      TVVLYNVFESFVTLG-GDAVTG-----VDCVKGIVSFFVVSLGGTLVGV-IFAFLLSLV
                                                                                                                                                                                                                --AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI-----LVGLAYFAAVLSMI 292
                                                                                                                                                                                                                                                           ----MGELKIGLLD----FLLFGSLIAAVDPVAVLAVFEEVHVNEVLFIIVFGESLLNDAV 220
                                                                                                                                                                                                                                                                                                                                             GNL-----GTI--LLYAVIGTIWNAATTGLSLYGVFLSGL------ 167
                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VLGLVLGGIV---WAADHIASFTLTPTLFFFYLLPPIVLDAGYFMPNRLFF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IVTFKWHHVQDPYIIALWILVASLAKIVF-----HLSHKVTSVVPESALLI------ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVMKWKTVSTIFLVVVLYLIIGAA--VFKALEQPQEISQRTTIVIQKQTFIAQHACVNS 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELDELIQQIVAAINAGIIPLGNSSNQVSHWDLGSSFFF------AGTVI-TTIGF 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
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1300 I Street, N.W., Suite 700
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PatentIn Release #1.0, Version #1.30
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                                                                                                                          ---SKKTKEEVGEFRAHAA 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 408 4400
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
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APPLICANT: Brant,
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SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
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                                                         223 TVVLYNVFQSFVTLG-GDKVTG-----VDCVKGIVSFF
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275 TRETKHVRVIEPGEVETISYLSYLTSEMLSLSSILAITECS CCOKYVKANISEQSATTV 334
                                   293 GDW---LRVI-----
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ZIP: 20005-3315
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                                                                                                                                                                                                                                                                                                                                                               43 IVTFKWHHVQDPYIIALWVLVASLAKIVF------HLS:HK:.SVVPESALL------- 87
                                                                                                                                                                                                                                                                                                                                                                                       39 INVMKWKTVSTIFLVVVLYLIIGAA--VFKALEQPQEIS AR HIVIQKQTFIAQHACVNS 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/677,734A FILING DATE: 10-JUL-1996
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                                                                                                                                                                                                                                                    GNISPRTEGGKIFCIIYALL------GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTF 196
                                                                                                          --AIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI-----LVGLAYFAAVLSMI 292
                                                                                                                                                                                                                                                                                                                       TELDELIQQIVAAINAGIIPLGNSSNQVSHWDLGSSFFF-------AGTVI-TTIGF 145
                                                                                                                                          ----MGELKIGLLD----FLLFGSLIAAVDPVAVLAVFEEVHVNEVLFIIVFGESLLNDAV 222
                                                                                                                                                                                                                                                                                        -----IVLGLVLGGIVL--AADHIASFTLTPTVFFFYLLPPIVLDAGYFMPNRLFF 136
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ilarity 19.8%;
Conservative 55
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Donowitz, Mark
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N: 435
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                                                                      ELGGTLVGVV-FAFLLSLV 274
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                                 -SKKTKEEVGEFRAHAA 315
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                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 408-440 (INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, VGCURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/677,734A
FILING DATE: 10-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                 223 VALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI----
                                                                    163
                                                                                                                                    127
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                                                                                                                                                                                                                                                                        Local Similarity
les 67; Conserv
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DAVTVVLYNVFESFVAL---
                                                                                       FGFLLAG-VGD-QLG----TIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILEG-CVLF 222
                                                                  YGYFLSGLMGDLQIGLLDFLLFGSLMAAVDPVAVL--AVFEEVHVNEVLFIIVFGESLLN 220
                                                                                                                                    AGYF - - - - MPNRLFFGNLGT ILLYAVVGTVWNA - - - - -
                                                                                                                                                                    AGIIPLGNSSNQVSHWDLGSSFFFA--GTVITTIGFGNISPRTEGGKIFCIIYALLGIPL 169
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FORDIS, Jean B.
FORDIS, Jean B.
FORDIS AND BER: 32,984
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Donowitz, Mark
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                                                                                                                                                                                                                                                                        Conservative
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___NO: 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05387.0043-00000
                                                                                                                                                                                                                                                                    Score 96.5; DB Pred. No. 0.24; 9; Mismatches
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   -GGDNVTGVDCVKGIVSFFVVSLG 260
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                                                                                                                                   -----ATTGLSL
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Brant, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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| 261 GTLVGVV-FAFLLSLVTRFTKHVRIIEPGFVFIISYLSY: ; EMLSLSAILAITFCGICC 319
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                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fordis, Jean B.
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VALPAVIEKHIEGWSALDAIYFVVITLTTIGFGDYVAGG
                              YGVFLSGLMGDLQIGLLDFLLFGSLMAAVDPVAVL--A
                                                             FGFLLAG-VGD-QLG----TIFGKGIAKVEDTFIKWNVS
                                                                                             AGYF----MPNRLFFGNLGTILLYAVVGTVWNA-----
                                                                                                                             AGIIPLGNSSNQVSHWDLGSSFFFA--GTVITTIGFGN1.
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5871919
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1300 I Street, N.W., Suite 700
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                         4.6%; Score 96.5;
20.4%; Pred. No. 0
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PRIOR APPLICATION NUMBER: EP 95201669.9
APPLICATION NUMBER: EP 95201669.9
FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
NAME: Fanucci A., Allan
NAME: Fanucci A., Allan
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                                                                                                                                                                                                                                                                                                                                   Query Match 4.6%; Score 96; DB 1; Length 473; Best Local Similarity 22.8%; Pred. No. 0.12; Matches 47; Conservative 33; Mismatches 52; Indels.
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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STREET: New York
STATE: New York
STATE: U.S.A.
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APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LACTIC BACTI
TITLE OF INVENTION: EXOPOLYSACCI
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221 DAVTVVLYNVFESFVAL----
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                                                                                                                                                                                                                                                     280 KSKYYSDVFHYLATFLLLGTSAFMIVLKP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION: 426
                                                                                                                                                                                                                                                                                        43 KWKTVSTIFLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDEL 102
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                                                                              TKGVFMTSIYGTIVCVLLQVVLLPIIGLDGAGLSAMLGFLTTF---LLRVKDT-QKFVVI 406
QIKWRIFISNLLIVLAQILCLFYLPS 432
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Search completed: August 28, 2001, 17:06:22 Job time: 526 sec

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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: pir2:*
3: pir3:*
4: pir4:*
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inward rectifier potassium channel TWIK-1 - humbun C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-19~~ *text_change 05-Nov-1999 C;Accession: S65566 C;Accession: F; Guillemare, E; Fink, M.; Duprat, A; Lazdunski, M.; Romey, G.; Barhani EMBO J. 15, 1004-1011, 1996 A;Title: TWIK-1, a ubiquitous human weakly inwar ** ctifying K(+) channel with a nove A;Reference number: S65566 A;Reference number: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65666 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65666 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65666 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65666 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65666 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Accession: S65566 A;Acc		hypothetical prote		potassium channel	probable potassium	hypothetical prote	hypothetical prote	potassium channe	potassium channel	hypothetical prote	hypothetical		hypothetical prote	hypothetical prote	£3357 7 546+

Ouery Match Best Local Similarity 32.5%; Pred. No. 5.3e; Matches 90; Conservative 62; Mismatches 1; Indels 17; Gaps 9; Qy 51 FLVVVLYLIGAAVFKALEQPQEISQRTTIVIOKQTTACVNSTELDELIOQIVA 108	RESULT T43509 probab C; Spec C; Date C; Acce R; Wang submit A; Desc	DЪ	Qy	Db	Qy	DЪ	Qy	Db	Qy	Db	Qy	Mato	Que
	RESULT 2 T43509 probable potassium channel chain n2P38 - Caenorhatditis elegans C;Species: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000. #text_change 21-Jan-2000 C;Accession: T43509 C;Accession: T43509 R;Mang, Z.W.; Salkoff, L. submitted to the EMBL Data Library, August 1998 A;Description: Potassium channels in C. elegans.	260 MLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE		200 AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYY "FIGHTCYLLLGLIA 259		144 FTLLFLTAVVQRTTVHVTRREVLYFHIRWGESKQVVAIVHAVLLGEVTVSCEFEIP 199	169 LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIKI 1FILFGCVLFVALP 226	ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGF: VPLSDGGKAFCIIYSVIGIP	AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIP		51 FLVVVLYLIIGAAVFKALEQPQEISQRTTTIVIQKQT' : .:ACVNSTELDELIQQIVA 108	ative 62; Mismatches : 1; Indels 17;	18.0%; Score 376.5; 1.7.

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R:Murray, J.; Wohldmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F34D6.
A;Reference number: Z21153
A;Reference number: Z21153
A;Reference number: T21153
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-329 <WAN>
A;Cross-references: EMBL:AF083652; PIDN:AAC32863.1
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                                                                                                                                                                             RTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIIS
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                                                                                                                      MTDAGKVFCMLYALAGIPLGLIMFQSIGERMNTFAAKLL----RFIRRAAGKQPIVTSS
                                                                                                                                                                                                                                       MSNA-DYEILEATIVKSVPHKAGY------QWKFSGAFYFATTVITTIGYGHSTP 108
                                                                                                                                                                                                                                                                                                                                                           MKRQNIRTLSLIVCTLTYLLVGAAVFDALETENEILQVRGLGEPRKLVQRVREKLKTKYN 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94;
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Pred. No. 3.4e-19;
63; Mismatches 95
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Pred. No. 2.7e-20;
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hypothetical protein KOlD12.4 - Caenorhabditis & ... C;Species: Caenorhabditis elegans C;pate: 15-Oct-1999 #sequence_revision 15-Oct-15.50 C;Accession: T23182 R;Dobson, R.
A; Experimental source: C; Genetics:
                                 submitted to the EMBL Data Library, June 1996
A; Reference number: Z19703
A; Recession: T23182
A; Status: preliminary; translated from GB/EMBL/DDRJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-383 <WILD
A; Cross-references: EMBL: Z75543; PIDN: CAA99871.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T13807
R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; T. Ch, M.H. R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; T. Ch, M.H. Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, T. Yu A;Title: ORKI, a potassium-selective leak channe two potassium-selective leak channe two potassium-selective leak channe two potassion: T13807
A;Accession: T13807
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C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-199; 'ext_change
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A;Map position: 1
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A; Residues: 1-1001 <GOL>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                          VGYLRRMLN-ELY
                                                                                                                                                                                                                                                                                                                                                             FKETRRRLSVEIY 337
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                  clone K01D12
                                                                                                                                                                                                                                                                                                                          310
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                                      CESP: K01D12.4
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A; Map position: 5 A; Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

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RESULT 6
T19860
T19860
hypothetical protein C40C9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #to
C;Accession: T19860
R;Hembry, C
                                                                                                                                                                                                                                                                                                            A;Cross-references: EME
A;Experimental source:
C;Genetics:
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A; Accession: T19860
A; Status: preliminary; translated fr
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A; Residues: 1-334 <WIL>
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Best Local Similarity
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:Introns: 34/1;
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Best Local Similarity
                                                                                                                                                                                                                                                                                               Gene: CESP:C40C9.1
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                             166 GIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIK-----wnvSQTKIRIIS-TIIFILFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVVLYLIIGAAVFKALEQPQEI
GVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLTIGFMV--
                                                                                         VAAINAGIIPLGNSSNQVSH-WDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                                                                                                          LILSTFTYLLFGAMVFDKLE-----SEKDTWVRDEIERITDRLKHK-YNFSERD----LHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQRTTI----VIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNSSNQVSHWDLGS
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                                                            FEAIAIKSIP-----QQAGYQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLFCMIFALF
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                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                            clone C40C9
                                                                                                                                                                                                   13.7%;
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Pred. No. 7.
                                                                                                                                                                                     Score 286.5; DB 2;
Pred. No. 1e-15;
8; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                          from GB/EMBL/DDBJ
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'.6e-16;
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                                                                                                                                                                                                                  Length 334;
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                                                                                                                                                                                                                                                                252/2;
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potassium channel chain n2P18 homolog - C;Species: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 2
                                                                                                                                                       RESULT
T43394
             A; Reference number: Z2;
A; Accession: T43394
A; Status: preliminary;
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A;Description: Potassium channels in C. elegans
A;Reference number: Z22450
A;Accession: T43361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable potassium channel chain n2P20 - Caenorhabe
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-20
                                        A;Description: Potassium channels
A;Reference number: Z22479
                                                                                   C; Accession: T43394
R; Kunkel, M.T.; Sal
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R; Wang, Z.W.; Salko
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                                                                     submitted to the EMBL Data Library,
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A; Residues: 1-364 <WAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z.W.; Salkoff, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                           GIPLEGELLAGVGDQLGTIFGKGIAKVEDTFIK-----WNVSQTKIRIIS-TIIFILEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAA
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                                                                                    M.T.; Salkoff, L.
                                                                                                                                                                                                                                                                      FILIGLAVESACVNLL--
                                                                                                                                                                                                                                                                                               WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHA/ WTANVTAEFKETRRRLSVEI 336
                                                                                                                                                                                                                                                                                                                                                                                      GVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLTIGFMV---
                                                                                                                                                                                                                                          YDKFQRATSVKRKL
                                                                                                                                                                                                                                                                                                                            ----IVSGTYMFHTIEKWSIFDAYYFCMITESTIGFGDI.VPLQQVNALQDQPLYVFATIM
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type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 28.7
90; Conservative
             translated
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              from GB/EMBL/D:
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                                                      August 1998
n C. elegans
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                                                                                                                                                                                                                                                                        -VLGFMASNADEVTA - - -
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                                                                                                               *text_change 21-Jan-2000
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                                                                                                                                          elegans
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A;Reference number: Z20027
A;Reference number: Z20027
A;Accession: T25392
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule: 1-393 <WIL>
A;Cross-references: EMBL:Z92813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T28A8.1
A;Cross-references: Clone T28A8
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change
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A; Introns: 73/1; 112/3;
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A; Cross-references: EMBL: AF083650; PIDN: AAC32861.1
                                                                                                                                                                                                                                                                                       A; Gene: CESP: T28A8.1
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                                                                                                                                                 Query Match 13.3
Best Local Similarity 27.5
Matches 83; Conservative
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                                                                    EMRESGIGQHVVEDLAVKYVDNVTRILFEAFDTHCIGAKHLRPGGEDEDY - - NWTYMTAL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TIIFILFGCVLFVALPAVIFKHIBGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYL 267
                                 --KQTFIAQHACVNST--ELDELIQQIVAAINAGII-----PLGNSSNQVSHWDLGSSF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TDNDLLETLIREE 405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VDPEEDPENNKKSFDAV - - ISRMNWSKRGLYYLLPDSQKKELAKQSEKKMGRKSIKIQ - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSFPISGLLLITVIWVIFCAVLFTFLEEWDFGTSLYFTLISFTTIGFGDILP--SDYDFM
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                                                                                                                                               13.3%; Score 279; DB 2; 27.5%; Pred. No. 5.1e-15; tive 51; Mismatches 106;
                                                                                                                                                                                   Length 393;
                                                                                                                                                 Indels
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A;Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3: :70/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; B raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M. B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D Nature 368, 32-38, 1994

A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer tock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A;Title: 2.2 Mb of contiguous uncleotide sequence from chromosome III of C. elega A;Reference number: 843531; MUID:94150718

A;Reference number: 843531; MUID:94150718

A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
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A; Residues: 1-392 <WIL>
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Best Local S
Matches 82
  332
                                      277
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YLMGGLCCMMLFLATLYD 349
                                                                        LDPKSAAQNS-----KPRLSFSSKPTVLAS----RVESD : INVMKWKTVSTIFLVVVLY 57
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                                      WILVGLAYFAAVLSMIGD
                                                                                                                                                       SAIVARMREPSHKLRGLLNQRLGHLF
                                                                                                                                                                                                                                                                                                                                                                                              LEPRTSAHQSSLYPVEPKMAIAKEMSFYSDQKIPKFHFFFSLKISKLKPAKNRY------ 117
                                                                                                                                                                                                                                                                                                                 -----FSRIEYPLEKIEREAYLDYQNQWRDRLIQLDIDESEIDKLFLNIREAALNG-- 168
                                                                                                                                                                                                                                                                                                                                                       LIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQ--HACVNSTELDELIQQI-VAAINAGI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLREKCSKQ--KYSVISSKDDKNKEGDLNLDHLENYIS (1 IFLIVAILLSYITFGAVVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGIAKVEDTFIKWNVSQTK-------IRIISHIFILFGCVL-FVALPAVIFK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FFTTTLLTTIGYGNLTPVTGRGKLLCILYALFGVPLILITVADIGKFLSENIVQLYTWYR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                              ----GDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.0%; Score 271; DB 2; Length 392; 25.8%; Pred. No. 2.3e-14; Live 65; Mismatches 109; Indels
                                      294
                                                                                                                                                       -- FVNHIQLIHVGV-VFASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID: g6434446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        III of C. elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.; Sonnhammer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                       271
                                                                                                                                                                                              219
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M.; Jo
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A; Molecule type: DNA
A; Residues: 1-522 <WIL>
A; Cross-references: EMBL: Z70036; P
A; Cross-references: clone T01B4
A; Molecule type: DNA
A; Residues: 1-325 <FAV>
A; Cross-references: EMB
                                            A, Accession: T15584
A, Status: preliminary; translated
                                                                                                                                                        hypothetical protein C24A3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t.C;Accession: T15584
                                                                                                                                                                                                                                                                                                                                                                  밁
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A; Introns: 95/3; 142/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data A; Reference number: Z19866 A; Accession: T24265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: R; Wilkinson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T01B4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                              Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated
                                                                                    A; Reference number: 218373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                          371 VNHLTSEREVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 IFLVVVLYLIIGAAVFKALEQPQE-----ISQRTTIVIQKQTFIAQHACVNSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                               NEHDSCQIEAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWIL--VGLAYFAAVLSMIGD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLEVFFEVPEDDKEDTTFQLRWG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KRCLELITKTFIQRSDEERGEGWRWDFWNSVFFSATIFTTIGYGNLACKTNLGRI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LILIILGYACLGGYMFQALEYDQQQLELEAEKRVRLSESSLLAVNLLEHLKQMNCGQSNE 100
                                                                                                                                                                                                                                                                                                                                                                                                                                    VENQYMWALELIDQKYQEKLKQDMYDEDEKKADKNDMHFSKKEPVRGPRILLQDLLRGPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAKV-----EDTF--IKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKHIEGWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTIYGMIGIPLMLFVLKNFGELCVKWAKKIQFNVQQCLKKCFGRKQKRASSLASITSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FCIIYALLGIPLFGFLLAGVGD-----
                                                                                                                                                                                                                                                                                                                                                                LKISGGRRSSSDASSVITEASDEDTRHFKVGRAILAEÅFAPDERASNHGTQLNSC--TVS
                                                                                                                                                                                                                                                                                                                                                                                                AEFKETRRRLS-----VEIYDKFQRATSVKRKLSAEL-----AGNHNQELTPCRRTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----W-LRVISKKTKEEVGEFRAHAAEWTANVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLTAFYFFFVSLSTIGFGDIVP------DHPRTACALFVLYFIGLALFAMVYAILQER 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDELIQQIVAAINAGIIPLGNSS-NQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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EMBL:U40424; NID:g1065542; PID:g1065543; PIDN:AAA81455.1; CESP:C24A3
                                                                                                                                                                                                                                                                                                                                 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224/3; 290/1; 458/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.9%;
23.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
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                                                    from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 270.5; DB 2
Pred. No. 3.5e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                  GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB/EMBL/DDBJ
                                                                                                                                                                       20-Sep-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------LLVIVLFVVLCSFVVSFWENWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136;
                                                                                                      C24A3
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                                                                                                                                                                                                                                                                                                                                                                                                                                    372
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hypothetical protein F19D8.1 - Caenorhabditis el. ...
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-199--
C:Accession. mollin
                                                                             Q
                                                                                                               B
                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-452 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data A; Reference number: Z19377 A; Accession: T21118
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A; Introns: 21/1;
               δõ
                                                Вb
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                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                           A; Map position: X
A: Introns: 31/1;
                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z78541; PIDN:CAB01740.1: C. PB:GN00028; CESP:F19D8.1
A;Experimental source: clone F19D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Swinburne, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: T21118
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Matches
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                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              :Gene: CESP:F19D8.1
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               193
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                                              146 VLFSFTILTTIGYGNVTPHTQQCKVFLMIYGAFGIPLFLITIADLGRFSKTAIMALVQKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILTTFQKTFKGLLPLIILVAYTLLGAWIFWMIEGENE---k, MLIEQQK------
            EDTFIKWNVSQTKIRIISTI----IFILFGCVLFVALPAV1FKHIEGW---
                                                                             FFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKV 192
                                                                                                               MNLKKDVIAKLATTENVAEINEHLRMFLRNISNLHISLDNYLIENEPTQIVPKRWTFPSS
                                                                                                                                              VIQKOTFIAQHACV-NSTELDELIQQIVAAINAGIIPLA: ----NSSNQV--SHWDLGSS 132
                                                                                                                                                                               KLKCNSKCAWMKFRNVLRIALGHLALYCFVVCYVFAGAWYFW JLEGENETELHDKQREYA 85
                                                                                                                                                                                                              RVESDSAINVMKWKTVSTI-----FLVVVLYLIIGAAVFKALEQPQEI----SQRTTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKGCKMLWRFFLK-----STRVVSKDLSNKISEAADN1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKGIAKVEDTFIKWNVSQTKIRIIS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HWTFLGSIFYCMTVYTTIGYGNIVPGTGWGRFATILYA: :f/'LTVLSLY----CLGSLF 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYAHLGIPLFGFLLAGVGDQLGTIF 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --ERDELIRRTVYKINQLQIKRQRRLMTAEEEYNRTAKVLTT;\QETLGIVPA--DMDKDI 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSFPISGLLLITVIWVIFCAVLFTFLEEWDFGTSLYFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity 25.4
87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --PIVGVLLLIGLSLVSTVMTLIQQQIEALASVRRRH
                                                                                                                                                                                                                                                                                                                               x
; 82/2; 101/3; 157/1; 197/1; 230/::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63/3; 131/1; 193/3; 206/3
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                               12.6%;
<del>..</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library,
                                                                                                                                                                                                                                                52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                                                                                              Score 263; DB 2;
Pred. No. 1.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.6; 4:
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                from
                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              August
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB/EMBL/DLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTIGFGDILP--SDYDFM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTAITPSAEKTENNDDDL
                                                                                                                                                                                                                                                                                                                                 .7/2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- AGIIPLGNSSNQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 325;
                                                                                                                                                                                                                                                                               Length 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ext_change 18-Feb-2000
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                                                                                                                                                                                                                                                                                                                                 325/3;
               -SALDAIYFV
                                                                                                                                                                                                                                              32;
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                                                                                                                                                                                                                                              Gaps
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hypothetical protein W06D12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T26229 R;Basham, V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F20Al.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T30037
R;Gattung, S.; Wu, X.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F20Al.
A;Reference number: Z20726
A;Accession: T30037
                                                                                                                           RESULT
T26229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Gene: CESP:F20A1.7
A:Map position: 5
A:Introns: 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1539 <GAT>
A;Cross-references: EMBL:U53150; PIDN:AAA96127.1; GSPDB:GN00023; CESP:F20A1
A;Experimental source: strain Bristol N2; clone F20A1
A;Experimental source: strain Bristol N2; clone F20A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KWNVSQ-----TKIRIIST-----IIFILFGCVLFVALPAVIF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AILKFEEDIGLEEPVIETVWTFWMSFLYAGTIFTTIGYGNIACKTRAGQIATMVYAFVGI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNSSNQVSHW-- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPTSLVASIK-ESAISSKRKLKYYCSFICTPIKKLLSTFKLLIIIGLYSFIGAHIFMYLE 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPTVLASRVESDSAIN---VMKW------KTVSTIFLVVV--LYLIIGAAVFKALE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKRELKKQSDEHLLREIAEVSPYLDVLLVAGLFVVFIAIGSAVIPLWENQLTYFDSVYFS
                                                                                                                                                                                                                                                                                                                                                                    MIGD-----WLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRL-----SVEIY 337
                                                                                                                                                                                                                                                                                                                                                                                                                  CLFEDWTFFTSFYFCFISLTTIGLGDVTPANPE----YMIATFGVVIVGLSMLTVCID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWKLSKHGAPSSIAISNSEENRLNSTPEDDEEEEEIHQDPPVLSTLIATVAWIILSAAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLF-----GFLLA------GVGDQ---LGTIFGKGI------AKVEDTFI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----DLG------SSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGI 167
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A;Gene: CESP:W06D12.2
A;Map position: 5
A;Introns: 70/3; 127/1; 170/1; 197/3; 326/1; 405/3
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A;Reference number: 20177
A;Accession: 73629
A;Status: preliminary; translated from GB/EMBL/DD:J
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A;Experimental source: clone W06D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-444 <WIL>
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Best Local Similarity
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53 VVVLYLIIGAAVF------KALEQPQEISQRTTIV164
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Search completed: August 28, 2001, 17:07:05 Job time: 474 sec

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Title:
Perfect score:
Sequence:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext
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TWK8_CAEEL
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CIQ1_MOUSE
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ORK1_DROME
CIW8_MOUSE
CIW7_HUMAN
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CIW4_HUMAN
CIW4_MOUSE
SSR5_MOUSE
NAH3_RABIT
COX1_RHEAM
Y718_METJA
MVIN_SYNY3
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ATCL_MYCPN
QOX1_BACSU
NAH3_DIDMA
YSY3_RHIME
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COBD_SYNY3
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MEMBKANE SION IN E KELETAL M PRESSION IUM. ACTI DIETHYI PORE DOM:	(APR-1999) to the EMBL/GenBank/DDI 1. 1. 254548; PubMed=10321245; . Honore E., Lesage F., Fink M., Popular anesthetics activate two-porces of the company o	ROM N.A., FÜNCTION, AND TISSUE SPECI- in; 157476; pubMed=9003761; 157476; pubMed=9003761; uprat F., Lesage F., Reyes R., Rome; functional expression and brain 1c, onal outward rectifier K+ channel. f; c6854-6862(1996).	CIW2_MOUSE STANDARD; PRT; 411 AA P97438; 01-CCT-2000 (Rel. 40, Created) 01-CCT-2000 (Rel. 40, Last sequence update) 01-CCT-2000 (Rel. 40, Last annotation update) 01-CCT-2000 (Rel. 40, Last annotation update) PPOTASSIUM CHANNEL SUBFAMILY K MEMBER 2 (OUTW): REC' CHANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM CHANNEL SUBGUNIT). KCNK2. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertina; Mammalia; Eutheria; Rodentia; Sciurognathi; Worldae NCBL_TaxID-10090;	97 4.6 602 1 CIK5_RAT 96.5 4.6 663 1 CNG2_BOVIN ALIGNMENTS	99 4.7 395 1 CDSA_MYCPN 98.5 4.7 520 1 TDT_BOVIN. 98.5 4.7 601 1 CIK5_MUSPF 98 4.7 305 1 CDSA_MYCGE 98 4.7 305 1 CIG4_HUMAN 97.5 4.7 602 1 TIRE_HAEIN 97.5 4.7 602 1 CIK5_MOUSE 97 4.6 579 1 TH83_SCHPO 07 4.6 602 1 CIK5_BAT
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-i- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH-
CHLOROFORM, HALOTHANE AND ISOFLURANE
-i- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN NAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Price L.A., Hellings S.E., Hayashi J.H., Pan. Th. M.H.; Submitted (MAY-1997) to the EMBL/GenBank/DDF.d ducabases -i- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
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603219; -
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two-pore-domain
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No. 1.7e-14
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ackground K+
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or send a
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED
STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK)
  InterPro;
InterPro;
                                                                                                                               modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restricted the companion of the companion of the control of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion
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                                               EMBL;
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                                                                                                                                                                                                                                                                                                              FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARD POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY). SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTESTMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF
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248242; AAG31731.1; ... 247042; AAF64062.1; ! ... IPR001622; -.. IPR003280; -..
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Catarrhini; Hominidae;
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OUTWARDLY R
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFANILY K MEMBER 4 (TWIKE RELATED STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
KCNK4 OR TRAAK.
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Patel A.J., Honore
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Mammalia; Eutheria;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
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PRINTS; PR01333; 2POREKCHANEL.
Ionic channel; Transmembrane; Ion transport; Potassium transport;
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                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
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SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND
2/TRAAKT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE.
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MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED ASSETTED ANAESTHETICS SUCH AS
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LFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTA
                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                      LVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTA 323
                                                               CVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI
                                                                                                     CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG
                                                                                                                    CIIYALLGIPLEGELLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILEG
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N-LINKED (GLCNAC. ...) (POTENTIAL).
KLLVE -> KAMAI (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
478A834B7B7AEC92 CRC64;
                                                                                                                                                                                                                                                                            Score 770.5;
Pred. No. 8e
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RESULT CINS_HWAN ID SCIUS_HWAN         Query Match
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01-0CT-2000 (Rel.
01-0CT-2000 (Rel.
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DOMAIN
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                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Ionic channel; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is probetween the Swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institute of Bioinforma and the swiss Institu
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Mammalia; Eutheria;
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Reyes R., Duprat F., Lesage F., Fink M., Salin s M.,
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SIMILARITY: BELONGS TO THE TWO PORE DOMAIN.
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SUBUNIT: HOMODIMER (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001622;
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                                 20.1%;
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                                 Score 420;
Pred. No. 8.
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ALSO DETECTED
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                                                             Desir G.V., Orias M., Freeman T.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
-!- SUBUNIT: HOMODIMER (POTENTIAL).
-!- SUBUNIT: HOMODIMER (POTENTIAL).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEYELS IN HEART BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
-!- MISCELLANEOUS: INHIBITED BY BARTUM, QUININE, QUINIDINE AND INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
-!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                            CIW1_HUMAN STANDARD; PRT; 336 AA.

000180; Q13307;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWARD RECTIFYING CHANNEL FROTEIN TWIK-1) (POTASSIUM CHANNEL KCNO1).

KCNK1 OR TWIK1 OR HOHO1 OR KCNO1.
                                                                                                                                                                                    Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.; "Sequence and function of the two P domain potassium implications of an emerging superfamily."; J. Mol. Med. 76:13-20(1998).
          This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                  "TWIK-1, a ubiquitous huma novel structure."; EMBO J. 15:1004-1011(1996)
                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                        MEDLINE=98122696; PubMed=9462864;
                                                                                                                                                                                                                                                      TISSUE-Brain,
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                                                                                                                                                                                                                                                                                                                     Barhanin J.;
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mare E., Fink M.
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or send a
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POTASSIUM CHANNEL SUBI
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EMBL; U76996; AAB97878.1;
EMBL; U90065; AAB51147.1;
MIM; 601745; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02034; TWIK_channel; 1. PRINTS; PR01096; TWIK1CHANNEL. PRINTS; PR01333; 2POREKCHANEL.
                            NCBI_TaxID=10090;
                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001622; -.
InterPro; IPR001779; -.
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    SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTF. 'JHACVNSTELDELIQQIVA 108
                                                                                                                                                                                                                                                                                                       AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGN SPRTEGGKIFCIIYALLGIP
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                                                                    (Mouse)
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                                                                                                 TWIK-1).
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40, Last sequence update)
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5UBFAMILY K MEMBER 1 (INW.)
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Rodentia;
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T->A: NO EFFECT '\ CHANNEL
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Sciurognathi; Y. dae;
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                                            Murinae;
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Query Match
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as none modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arrighi I., Lesage F., Scimeca J.-C., "Structure, chromosome localization, a mouse twik K+ channel gene."; FEBS Lett. 425:310-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurles Lazdunski M.;
"The structure, function and distribution of the mouse TWIK-l
                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01096; TWIK1CHANNEL. PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF033017; AAC16973.1; MGD; MGI:109322; Kcnkl.
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InterPro; IPR000099; .
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SUBBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESION IN BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL MUSCLE, THYMUS AND SPLEIN. IN THE BRAIN, HIGHEST EXPRESSION IN CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
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STABILIZES AFTER DAY
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                           FLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVA 108
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FLVLGYLLYLVFGAVVFSSEELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE 84
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                                                                                                                                                         Œ.
                                                                72;
                                                                 Score 370; DE
Pred. No. 1.5e
72; Mismatches
                                                                                                                                                       N-LINKED (GLCNAC. . .) (I
A996060A18266FD4 CRC64;
                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                             PORE-FORMING
                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                   PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                      Ion transport; Potassium
                                                                                  370;
No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINASE C.
DOMAIN FAMILY
                                                                                  DB 1;
.5e-18;
                                                                                                                                                                                                                                                                                                 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage,
                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND INTERNAL
                                                                 Indels
                                                                                                                                                                          (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 restrictions
                                                                                                                                                                                                                                                                                                                                                                    transport;
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                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
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O14649;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM
CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).
                                                                                                                                                                                                     +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Kidney;
MEDLINE=97459932; PubMed=9312005;
                                                                                                                                                                        -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                "Inhalational anesthetics activate two pore-
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99254548; PubMed=10321245; Patel A.J., Honore E., Lesage F., Fink M., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCNK3 OR TASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "TASK, a human background K+ channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duprat F., Lesage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109
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                                                                                                                                                                                     ION CONCENTRATION ON EITHER SIDE OF THE MEBBANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL). TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST EXPRESSION IN PANCKRAS AND PLACENTA. LOWER EXPRESSION IN BRAIN, LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SMALL INTESTINE AND COLON. MISCELLANBOUS: INHIBITED BY EXTERNAL ACTIVATED BY HEALOTHANE AND ISOFLURANE.
                                                                                                                                                                                                                                                                                                                                  FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION BYSULTS FROM POTASSIUM
                                                                                                                                                         CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                physiological pH.";
J. 16:5464-5471(1997).
                                                                                                                                                                                                                                                                                                                                                                     Neurosci.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVKRKLSAELAG -- NHNQELTPCRRTLSVNHLTSEREVLPP' LKAES - IYLNGLTPH 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVIFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGLAY
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                                                                                                                                                                                                                                                                                                                                                                      2:422-426(1999).
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                                                                                                                                                                        BELONGS TO THE TWO PORE DOMA THE FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F., Fink M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Heurteaux C., Lazdunski M.; sense external pH variations
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                                                                                                                                                                                                                                                                                                                                                                                                 y G., Lazdunski
ain background
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ackground K+
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                                                                                                                                                                                                                                                                                                                                                    POTASSIUM
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CIW3_MOUSE
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Best Local :
                                                        CHWI_MOUSE STANDARM:

O35111; O35163;

O1-OCT-2000 (Rel. 40, Created)

O1-OCT-2000 (Rel. 40, Last sequence update)

O1-OCT-2000 (Rel. 40, Last annotation update)

POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL POTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K-CHANNEL)

CHANNEL POTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K-CHANNEL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ionic channel; Transmembrane;
Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01095; TASKCHANNEL. PRINTS; PR01333; 2POREKCHANEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02034; TWIK_channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003092;
InterPro; IPR003280;
SEQUENCE
                                Mammalia;
                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000099; InterPro; IPR001622;
                    NCBI_TaxID=10090;
                                                                                                                                                                                                              335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 MKWKTVSTIFLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNS--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                      musculus
                                                                                                                                                                                                            QRATSVKRKLSAELAGNHNQELTPCRRTL 369
| | | : | : | | | | | | | |
TSDTCVEQSHSSPGGGGRYSD-TPSRRCL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                    ELERVVLRL-KPHKAGV------OWRFAGSFYFAITVITTIGYGHAAPSTDGGKV
                                                                                                                                                                                                                                                                              GEFRAHAAEWTA------
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                                                                                                                                                                                                                                                                                                              ANMVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT
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                                                                                                                                                                                                                                                         GGGSAHTTDTASSTAAAGGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLS
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FROM N.A
                               Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394
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108
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244
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                                                     (Mouse)
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101
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                               Chordata;
Rodentia;
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28.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 370;
Pred. No. 1
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9FF4C8266F615FB7 CRC64
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POTENTIAL.
PORE-FORMING (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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                                         Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ion
                               Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transport;
                                          Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; L
1.8e-18;
hes 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                          Euteleostomi;
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                                Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88;
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MEDLINE-20287574; PubMed=10748056; Lopes C.M., Gallagher P.G., Buck M.E., Butlc & .H., Golds "Proton block and voltage gating are potassi", lependent cardiac leak channel konks.";
J. Biol. Chem 275.1600.
                                            CONFLICT
CONFLICT
SEQUENCE
                                                                                   DOMAIN
CARBOHYD
                                                                                                            DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. BIOL. Chem. 275:16369-16378 (2000).

-i- EUNCTION: PH-DEPRIDENT, VOLTAGE-INSENSIT, I, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION, SULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE STRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSI' ONCENTRATION IS LOW.

WHEN EXTERNAL POTASSIUM CONCENTRATION I
                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See ling://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97459932; PubMed-9312005;
Duprat F., Lesage F., Fink M., Reyes
"TASK, a human background K+ channel
near physiological pH.";
EMBO J. 16:5464-5471(1997).
                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB008537; BAA25436
EMBL; AF006824; AAC53367
EMBL; AB013345; BAA28349
EMBL; AF241798; AAF81418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Circ.
                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                   PRINTS; PRO1095; TASKCHANNEL. PRINTS; PRO1333; 2POREKCHANEL. Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                             EMBL; AF242508; AAF8141 MGD; MGI:1100509; Kcnk3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim D., Fujita A., Horio Y., Kurachi Y.; "Cloning and functional expression of a background K+ channel (CTBAK-1)."; Circ. Res. 82:513-518(1998).
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                        Glycoprotein
                                                                                                                                                                                                                                                                            Pfam; PF02034; TWIK_channel; 1.
                                                                                                                                                                                                                                                                                        InterPro; IPR003092; -
InterPro; IPR003280; -
                                                                                                                                                                                                                                                                                                                 InterPro; IPR000099; -. InterPro; IPR001622; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 4-409 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98165556; PubMed=9506712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE. FIELN (POTENTIAL).

TISSUE SPECIFICITY: VERY STRONG EXPRESS: FIN HEART, ALSO DETECTING EXPRESS: FIN HEART, ALSO DETECTING STATEMENT, SKIN, TESTIS, LUNG, SK. FETAL MUSCLE, SMALL INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN MISCELLANEOUS: INACTIVATED BY BARIUM.

SIMILARITY: BELONGS TO THE TWO PORE DOMALE CAMILLY OF POTASSIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHANNELS
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108
129
159
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244
53
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; AAC53367.1;
; BAA28349.1;
; AAF81418.1;
                                                                                                                                                                                                                                                                                                                                               Kcnk3
                                                         29
101
128
158
179
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243
409
53
                                               ¥.
                                                      POTENTIAL.
CYTOPLASMIC (POTE: flat).
N-LINKED (GLCNAC...) (POTE: flat).
V-> E (IN REF. 2...)
V-> I (IN REF. 2...)
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                                                                                                                                                                                                                                                                                                                                                           JOINED
                                                                                                                        CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PORE-FORMING (POTENTIAL)
                                                                                                                                                                   POTENTIAL
                                                                                                                                                                              POTENTIAL.
PORE-FORMING
                                                                                                                                                                                                          CYTOPLASMIC
                                            35236E011AAC5f+
                                                                                                                                                                                                                                    transport;
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CRC64:
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external
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                                                                                   (POTENTIAL)
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pH variati
                                                                                                                                                                                                                                    transport;
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InterPro;

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RESULT 1
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Best Local
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01-CCT-2000 (Rel. 40, Created)
01-CCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ C
                                     use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        Leonoudakis D., Gray A.T., Winegar B.D., Kindler C. Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S. "An open rectifier potassium channel with two pore
                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Cerebellum;
MEDLINE=98099797; PubMed=9437008;
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  InterPro;
                                                                                                                                                                                                                                                                                                                                              cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                 ned from rat cerebellum.";
Neurosci. 18:868-877(1998).
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                                                                                         ween the Swiss Institute of Bioinformatics 
European Bioinformatics Institute. There
                                                                                                                                                                                                (BY SIMILARITY).

(BY SIMILARITY).

SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE

EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AN
                                                                                                                                                                                                                                                                            FUNCTION: PH-DEPENDENT VOLTAGE-INSENSITIVE, BACKGROUND POTASSI
CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
                                                                                                                                             SIMILARITY: CHANNELS.
                                                                                                                                                                                    MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC,
                                                                                                                                                                      BUPIVACAINE
                                                                                                                                                                                                                                                                 WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright.
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               AF031384;
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             AAC39952.1;
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Rodentia;
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31.1%;
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Sciurognathi;
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                                                               Usage
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                                                                  and
                                                                                                     EMBL
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                                                                                                          a collaboration
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RESULT 11
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AC Q9Y257
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Best Local s
Matches 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
                                  FEBS
[2]
                                        Pountney D.J., Gulkarov I., Vega-Saenz de M. Saganich M., Rudy B., Artman M., Coetzee W., "Identification and cloning of TWIK-origina-(TOS5): a novel human 2-pore K+ channel pri: FEBS Lett. 450:191-196(1999).
                                                                                                                                                              CHANNEL PROTEIN TWIK-2) (TWIK-ORIGINATED SINGLE RITY SEQUEN KCNK6 OR TWIK2 OR TOSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02034; TWIK_channel; 1
PRINTS; PR01095; TASKCHANNEL
PRINTS; PR01333; 2POREKCHANEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
              TISSUE=Brain;
                      SEQUENCE FROM N.A., AND
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                 Eukaryota;
                                                                                                                                                           Homo sapiens
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                                                                                         MEDLINE=99285568; PubMed=10359073;
                                                                                                   FISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                              EYLDEYKPVVWEWILVGLAYFAAVLSMIGDWLRVISKK **K; VGEFRAHAAEWTAN
                                                                                                                                                                                                                                                                                     QTQPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMN
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                                                                                                                                                                                                                                                                                                                                                                                                                     D-ELIQQIVAAI----NAGIIPLGNSSNQVSHWDLGSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                        ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001622;
IPR003092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR003280;
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78
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     PubMed=10075682
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Primates;
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31.1%;
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                                                      sequence
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SEQUENCE
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J. Biol. Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       potassium channel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ionic channel;
                                                                                                              173
                                                                                                                                                                                      117
                                                                                                                                                                                                                                                                                               Local Similarity
nes 83; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES
TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN
PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED
IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOWEST EXPRESSION DETECTED IN BRAIN.

MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARIUM. SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHANNELS
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                     KHI-EGWSALDAIYFVVITLITTIGFGDYVAGGSDIE-YLDFYKPVVWFWILVGLAYFAAV
                                                                                                                                                                     LGNSSNQVS----HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGF
                                                                                                                                                                                                                                                            YLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIP 116
AHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALYKVLVTVYLFLGLVAMVLV
                                                                                                            LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVA--LPAVIF
                                                                                                                                                 LANASGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTML 136
                                                                                                                                                                                                                       YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCVAAPALDAFVERVLAAGRLGRVV 76
                                                                         LLTASAQRLSLL----LTHVPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCFLVPAVIF
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Y., Forsayeth J.R., Yost C.S.;
l. Chem. 274:24440-24440(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR01096;
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274:7887-7892(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
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., Yost C.S.;
                                                                                                                                                                                                                                                                                                                                                                                             MW.
                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                   Score 342; DB 1;
Pred. No. 1.1e-16;
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N-LINKED (GLCNAC...) (POTENTIAL).
C->A: NO CHANNEL ACTIVITY.
; 1379382DFB0575DE CRC64;
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CYTOPLASMIC (POTENTIAL).
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PORE-FORMING
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PORE-FORMING
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RA Dodson K., Dowp L.E., Downes M., Dugan-Rocha J. Dunbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Felschmann W., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferraz C., Felschmann W., RA Burbin K.J., Evangelista C.C., Ferraz C., Felschmann W., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan F., Harris M., Ra Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei F., H. Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei F., H. Ibegwam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A., RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz.S., Kulp D., Lai Z., Ra Liu X., Mattei B., McIntosh T.C., McLeod M., Hocherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morres J., Moshrefi A., RA Menton G.S., Molson K.A., Nixon K., Nusskein D.R., Pacleb J.M., RA Mount S.M., Welson K.A., Nixon K., Nusskein D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard D.R., Pacleb J.M., Ra Menert K., Remington K., Samders R.D.C., Sheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skugski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Ra Zheng X.H., Zhong W., Rubin G.M., Venter E., Wang A.H., Wang S., Yao Q.A., RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., RA Zheng R.A., Myers E.W., Rubin G.M., Venter J. C., The Genome sequence of Drosophila melanogusjer."

"The genome sequence of Drosophila melanogusjer."
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Adams M.D., Celniker S.E., Li P.W., Hosk h. R.A., Galle R.F.,
Adams M.D., Celniker S.E., Li P.W., Hosk h. R.A., Galle R.F.,
Adams M.D., Celniker S.E., Richards S., Ashburnyi M., Henderson S.N.,
Adams G.G., Wortman J.R., Yandell M.D., Zhaiv, Q., Chen L.X.,
Adams R.G., Rogers Y.-H.C., Blazej R.G., Olimpe M., Pfeiffer B.D.,
Adams K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Adams M.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Adams M. H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Adams M. H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-1, Ginkoch C., Baldwin D.,
Adams M. H., Basu A., Baxendale J., Bayrakt., W. U., Beasley E.M.,
Adams M. H., Benos P.V., Berman B.P., Bhand, W. L., Bolshakov S.,
Beson K.Y., Benos P.V., Berman B.P., Bhand, W. J., Brottler P.,
Adams K.C., Busam D.A., Butler H., Cadieu 1, Ginter A., Chandra I.,
Adams M. Cawley S., Dahlke C., Davenport. 3, Davies P.,
Adams M. J., Brotter M., Deng Z., Mays A.D., Dev I., Dletz S.M.,
Adams M. J., Brotter M., Deng Z., Mays A.D., Dev I., Dletz S.M.,
Adams M. J., Brotter M., Deng Z., Mays A.D., Dev I., Dletz S.M.,
Adams M. J., Brotter M., Deve J., Mays A.D., Dev I., Dletz S.M.,
Adams M. J., Brotter M., Deve J., Davies P.,
Adams M. J., Brotter M., Deve J., Deve J., Dletz S.M.,
Adams M. J., Brotter M., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J., Deve J.,
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MEDLINE-20196006; PubMed-10731132;
Aniker S.E., Holt R.A.
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GORKI, a potassium-selective leak channel with two pore domains
"Conned from Drosophila melanogaster by expression in Saccharomyces
"Connection of the Connection of the C
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ORK1 OR CG1615
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TISSUE SPECIFICITY: WIDESPREAD
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PORE-FORMING
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EAD EXPRESSION IN ADULT, STRONGEST
AND OVARY. ALSO PRESENT AT LOW LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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No. 5.7e-15;
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"Cloning of a tesis."
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Q9Z2T1; Q9R242; Q9R1V1; Q9QYE8; Q9QXYO;

01-OCT-2000 (Rel. 40, Created)

01-OCT-2000 (Rel. 40, Last sequence update)

01-OCT-2000 (Rel. 40, Last annotation update)

POTASSIUM CHANNEL SUBFAMILY K MEMBER 8 (PUT... I'v POTASSIUM CHANNEL

DP3) (DOUBLE-PORE K+ CHANNEL 3) (NEUROMUSCULAR FWO P DOMAIN POTASS.
                                                                                                                                                                                                                                                                                           This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gan L., Joiner W.J., Quinn A.M.,
Kaczmarek L.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                    or send an
                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bockenhauer D., Nimmakayalu
Gallagher P.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain, and MEDLINE=99223496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 2-307 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-289
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                                                                                                                                                                                                                                                                                                                                                                              REACH THE PLASMA MEMBERS.
SUBUNIT: HOMODIMER (POTENTIAL).
TISSUE SPECIFICITY: DETECTED IN EMBRYO, TISSUE SPECIFICITY: DETECTED IN EMBRYO, TESTIS, ATHIE, WEAKLY EXPRESSED IN COLON, TESTIS, ATHIE, THE YEAR STEM. DETECTED IN BRAIN, CEREBELLUM, SPINAL C. STEMEN, VENTRICLE, DETECTED IN BRAIN, CEREBELLUM, SPINAL C. FEART, VENTRICLE, SKELETAL MUSCLE, LIVER, PLACENTA AND PANETY S. IN THE EYE, HIGH FXPRESSED IN THE RETINAL GANGLION CELL LANGE AND INNER NUCLEAR FXPRESSED IN THE RETINAL GANGLION CELL LANGE AND INNER NUCLEAR
                                                                                                                                                                                                                                                                                                                                               LAYER.
SIMILARITY:
CHANNELS.
                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is producen the Swiss Institute of Bioinformati;
                        AF110521;
AB015729;
                                                                                                          non-profit institutions as long
and this statement is not removed
requires a license agreement (See
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       localization, channel KCNK6
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new double-pore
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274:11751-11760(1999).
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BAA35074.1;
AAD09337.1;
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PubMed=10206991;
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information and the EMBL
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Q1-OCT-2000 (Rel
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Q1-OCT-2000 (Rel
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Lazdunski M.;
"Cloning of a nu
homologue with
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR003280;
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EMBL; AF158234; AJ
MGD; MGI:1341841;
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                                                                   MEDLINE-99223496;
                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                         KCNK7
                                                                                     TISSUE-Brain;
                                                                                                                                                                                                                         POTASSIUM CHANNEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CVLFVALPAVIFKHIEG-WSALDAIYFVVITLTTIGFGDYV-AGGSDIEYLDFYKPVVWF
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Similarity 29.6%;
84; Conservative (
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(Rel.)
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Rel. 40, Last sequence upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotation upon Rel. 40, Last annotati
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AAF14528.1;
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                                                                                                                                                                                                                       SUBFAMILY K MEMBER
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Primates;
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CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL)

NGS -> TR (IN REF. 4).

GS -> TR (IN REF. 4).

GS -> THSREFGPRGEEFGTR (IN REF. 2).

GS -> GS -> THSREFGPRGEEFGTR (IN REF. 2).

T -> P (IN REF. 2).

MW; 567D32AE355BA44F CRC64;
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Pred. No. 3.5e-14;
5; Mismatches 94;
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CYTOPLASMIC ()
POTENTIAL.
PORE-FORMING
 structure
                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PORE-FORMING
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                domain channel
                                                Fosset M.,
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on update)
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                                                                                                                                                     Hominidae;
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                subunit
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                                                                                                                                                                     Euteleostomi;
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                and
                                                 C.,
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                                                Romey
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Best Local S
Matches 88
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EMBL; AF11052
MIM; 603940;
                                                                                                                                                                                                                                                                                         VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                         VARSPLIC VARSPLIC
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics, and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as a content is in no was modified and this statement is not removed. It is and for commercial entities requires a license agreement (See hiti://www.isb-sib.ch/announce
                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [onic channel;
                                             183
                                                                                          126
 237
                                                                  223
                                                                                                               163
                                                                                                                                                            103
                                                                                                                                       67
                                                                                                                                                                                                         44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOL Chem. 274:11751-11760(1999),
FUNCTION: PROBABLE POROSSUM CHANNEL
OBSERVED IN VITRO AS PROTEIN REMAINS
MAY NEED TO ASSOCIATE WITH AN AS YET
                                                                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
ALTERNATIVE PRODUCTS: 3 ISOFORMS: A (SHC
PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE TWO PORE DOW!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REACH THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF110522;
AF110524;
AF110523;
ALLGYLLLGL - - -
                                                                 VALPAVIFKHIEG-WSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWF----
                                                                                                               ALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVFJTKIRIISTIIFILFGCVLF
                                                                                                                                                                                  WSRYGLLVVAHLLALGLGAVVFQALEGPPACRLQAELRAEI
                                                                                                                                                                                                         WKTVSTIFLVVVLYLIIGAAVFKALEQPQEISQRTTIVICK, FIAQH-ACVNSTELDEL
                   ----WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFR/. HAAEW--TANVTAE 324
                                           VLLPALVLWGLQGDCSLLGAVYFCFSSLSTIGLEDLLPG
                                                                                        AALGLPASLALVATLRHCLLPVLSRPRAWVA---VHWQLSFARAALLQAVALGLLVASSF
                                                                                                                                       LGTALATQAHGVSTLGNSS-EGRTWDLPSALLFAASILT TI
                                                                                                                                                 Similarity
88; Conserv
                                                                                                                                                                                                                                                                                     258
307
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                           253
241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternative
                                                                                                                                                                                                                                                                                          À,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane;
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; AAD29580.1;
; AAD29579.1;
                                                                                                                                                                                                                                                                                                                           307
257
                                                                                                                                                                                                                                                                                          31946
                                                                                                                                                                                                                                          14.4%;
                                                                                                                                                                                                                                                                                          MW;
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                                                                                                                                                                                                                                  60;
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                                                                                                                                                                                                                              Score 300.5; DB
Pred. No. 7.6e-14
60; Mismatches .!!
---LAVETFSELPQVRAMGKFFRPSGPVTAE
                                                                                                                                                                                                                                                                                                   YLLLGLLAMLLAVETPS -> (IN ISOFORM C)
MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                     PORE-FORMING (POT: VITAL)
POTENTIAL.
CYTOPLASMIC (POTH: TIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                               PORE-FORMING POTENTIAL.
                                                                                                                                                                                                                                                                                                                                       MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                              YLLLGLLAMLLA
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                                                                                                                                                                                                                                                                                                                                                             (GLCNAC...) (POTENTIAL)
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> KSSHLTACGGRGKRSLD
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RESULT 15

18;

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TRANSMEM CONFLICT
                                   TRANSMEM
TRANSMEM
                                                          TRANSMEM TRANSMEM
                                                                                           TRANSMEM
TRANSMEM
                                                                                                                                        PIR;
PIR;
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EMBL;
EMBL;
EMBL;
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P40310; Q05721;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
01-FEB-1995 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
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"Sequence and function analysis of a 9.46 kb
Saccharomyces cerevisiae chromosome X.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                 "The S. cerevisiae outwardly-rectifying | identifies a new family of channels with Recept. Channels 4:51-62(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guy H.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A new family of outwardly rectifying potassium channel proteins with two pore domains in tandem.";
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TOK1 OR DUK1 OR YJL093C OR J0911
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mitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
mitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
mitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
mitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
DOMAIN: SEEM TO BE COMPOSED OF TWO PORES.
                                                                                                                                       $46585; $46585.
$47058; $47058.
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Z49368;
U28005;
X94403;
U37254;
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O9es08 rattus norv
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Q9hb59 homo sapien
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Q9jk62 mus musculu
Q9z2t2 rattus norv
Q0z821 oryctolagus
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Q9hbc8 homo sapien
Q9j158 cavia porce
Q9qx34 mus musculu
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Q9h592 homo sapien
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J. Biol. Chem. 275:17412-17419(2000)
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MEDLINE=20298807; PubMed=10747911;
Bang H., Kim Y., Kim D.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             60.1%; Score 1256.5; DB 11; 65.3%; Pred. No. 1.1e-83;
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Q9HB59;
Q1-MAR-2001 (TrEMBLrel. 16, C
Q1-MAR-2001 (TrEMBLrel. 16, L
Q1-MAR-2001 (TrEMBLrel. 16, L
2P DOMAIN POTASSIUM CHANNEL T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20435789; PubMed=10880510;
Lesage F., Terrenoire C., Romey G., Lazdunski ...

"Human TREK2, a 2P domain mechano-sensitive K.: hannel with multiple regulations by polyunsaturated fatty acids, 1.-phospholipids and Gs, Gi, and Gq protein-coupled receptors.";
J. Biol. Chem. 275:28398-28405(2000).

EMBL; AF27890; AAG15191.1; -.

Ionic channel.

SEQUENCE 538 AA; 59764 MW: REAGISDOON.
                                           Q9H591;
Q9H591;
01-MAR-2001
01-MAR-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertel: ıta;
Mammalia; Eutheria; Primates; Catarrhini; Homi idae;
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                                                                                                                                                                                                                                                                                                                      KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFY. PVVWEWILVGLAYFAAVL 289
                                                                                                                                                                                                                                                      NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISFI 3GKIFCIIYALLGIPLF 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQH&VNSTELDELIQQIVAAI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAPDLLDPKSA------AQNSKPRLSESSKPTVLASRVE\)S---AINVMKWKTVSTI
                                                                                                                                                                                                                   -KRKLSAELAGNHNQELTPCRRTL
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                                            (TrEMBLrel.
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                                                                                                PRELIMINARY;
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16,
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; Pred. No. 2.56
54; Mismatches
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Last annotation updat
TREK2.
Last sequence upda(a)
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Best Local :
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                                                                                                                                                                                                                       POTASSIUM Chan...
Mus musculus (Mouse).
Mus mvota; Metazoa; Chordata;
--harvota; Rodentia;
                                                    Cid L.P., Niemeyer M.I., Sepulveda F.V.;
"Functional properties of mouse TASK-2 potassi
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
EMBL; AF259395; AAF68668.1; -.
EMBL; AF319542; AAG35065.1; -.
                                                                                                                                                              STRAIN=129/SVJ; TISSU
Roux J., Barhanin J.;
"Mouse two P domain p
                                                                                                                                                                                                                                                                  01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update
POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).
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                                                                                                                                                                                                                                                                                                                  <u> 0</u>9JK62;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001
DJ137F1.2 ()
 SEQUENCE
                               InterPro; IPR001622; InterPro; IPR003280;
                                                                                                                TISSUE-KIDNEY;
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                   Submitted (APR-2000)
                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLPLILAYVCYLLIGATIFQLLERQAEAQSRDQFQLEKLRFLENYTCLDQWAMEQFVQVI 73
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            channel
                    PR01333;
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                       2POREKCHANEL
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Primates;
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55976 MW;
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                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 499.5;
Pred. No. 7.3
                                                                                                                                                              channel TASK2.";
                                                                                                                                                                                                                                 Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FCBA3B352F1F0952 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
E4C7E7CC71B44D95 CRC64;
                                                                                                                                                                                                                                                                                                                              502
                                                                                        potassium channel.";
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                                                                                                                                                                                                                                            Euteleostomi;
                                                                                                                                                                                                                                  Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13;
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Best Local S
Matches 99
                                                                                               Matches
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Best Local
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Q9Z2T2;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                        PUTATIVE rolling (Rat).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertel ita; E
Eukaryota; Metazoa; Chordata; Sciurognathi; Mridae;
                                                                                                                                                                             InterPro; IPR003280; --
Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01096; TWIK1CHANNEL.
                                                                                                                                                                                                                                 Submitted (SEP-1997) to the EMBL; AF022819; AAD09336.1; InterPro; IPR000099; -. InterPro; IPR001622; -. InterPro; IPR001779; -.
                                                                                                                                                            Ionic channel. SEQUENCE 336
                                                                                                                                                                                                                                                                                                                                                                                                                          PUTATIVE POTASSIUM CHANNEL TWIK.
                                                                                                                                                                                                                                                                                                 two P domains."
                                                                                                                                                                                                                                                                                                                          Kaczmarek L.K.;
                                                                                                                                                                                                                                                                                                                                   Gan L., Joiner W.J.,
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            "Cloning and localization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186
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                        109
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 85
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                                                                       FLVV---VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTI:1AQ::ACVNSTELDELIQQIVA 108
              AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGWISPRTEGGKIFCIIYALLGIP
                                               FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELAGNHNQELTPCRRTLSVNHLTSEREVLPPLLK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETREE. F.EIYDKFQRATSVKRKLSA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIIST1.F1LFGCVLFVALPAVIFKHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAITGNOT--FUNWUWPNAMIFAATVITTIGYGNVAPKI, AGRLFCVFYGLFGVPL---C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRY ...XXIFCIIYALLGIPLFGFL
 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTWI-SALGKFFGGRAKRLGQFLTRRGVSLRKAQITCTA OVWGVLVHLVIPPFVFMVT
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                                                                                                           Similarity
                                                                                                                                                                                                                      IPR003280; -
                                                                                                                                                                                                                                                                                                                                                                                                                               (TrembLrel. 10, Created)
(TrembLrel. 10, Last sequence upar (TrembLrel. 16, Last annotation up
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                            38228 MW;
                                                                                                          18.0%;
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                                                                                               62;
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                                                                                              Score 375.5; DB H
Pred. No. 9.4e-20;
2; Mismatches 10H,
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Pred. No. 5.
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                                                                                                                                                            5E78031947D750E6
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... LSDGGKAFCIIYSVIGIP
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                                                                                               Indels
                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                       Murinae;
                                                                                                                                                                                                                                                                                                             channel
                                                                                               17;
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 78
                                             Q9HBC8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TWO PORE POTASSIUM CHANNEL KT3.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DOUBLE PORE POTASSIUM CHANNEL RABKCNK1 (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Lagomorpha; Leporidae; Oryctola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
PRINTS; PR
PRINTS; PR
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                         Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                         09нвс8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orias M., Velazquez H., Tung F., Desir G.V.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ
EMBL; AF004695; AAB61602.1; -.
InterPro; IPR001622; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      002821;
 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                   145
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                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                51 FLVV--VLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVA 108
                                                                                                                                                                                                                                                                                                                                                           26
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                     IFKHIE-GWSALDAIYFVVITLTTIGFGDYVAG-GSDIEYLDFYKPVVWFWILVGL
                                                                                                                                                                                                                                                                                                                     AINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIME 295
                                                                                                                                                                                          VFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGL
                                                                                                                                                                                                                                                FTLLFLTAVVQRVTVHVTR--RPVLYFHVRWGFSKQVVAIVHAVLLGLITVSCFFFIPAA
                                                                                                                                                                                                                                                                         LFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAV 228
                                                                                                                                                                                                                                                                                                    ANNYGVSVRSNASGN-WNWDFASALFFASTVLSTTGYGHTVPLSDVGKAFCIIYSVIGIP
                                                                                                                                                                                                                                                                                                                                                          FLVLGYLLYLVFGAVVFSSVELPYEDILTRQELTKLKTRFVEEHECLSEQQLEQFLGRVLE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCYLLLGLIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTLLFLTAVVQRVTVHVTR---RPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFI--P
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                                                                                                                                                                                                                                                                                                                                                                                                                 78;
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259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                         PRELIMINARY;
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29311 MW;
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33.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 353.5;
Pred. No. 2.7e
57; Mismatches
                                                                                                                         PRT;
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94;
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Best Local
                                                                   extracellular histidine as pH sensor.";
J. Biol. Chem. 275:16650-16657(2000).
EMBL; AF212827; AAF63706.1; -.
InterPro; IPR001622; -.
InterPro; IPR001622; -.
                                                                                                                                                                                                                                                                                   O9JL58; PRELIMINARY;
O9JL58; O1-OCT-2000 (TrEMBLrel. 15,
O1-OCT-2000 (TrEMBLrel. 15,
O1-MAR-2001 (TrEMBLrel. 16,
Pfam; PF02034; TWIK_Channel; 1. PRINTS; PR01333; 2POREKCHANEL. PRINTS; PR01095; TASKCHANNEL. SEQUENCE 365 AA; 40769 MW;
                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                      Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                             InterPro; IPR003092; InterPro; IPR003280;
                                                                                                                                          Rajan S., Wischmeyer
Karschin A., Derst C.
                                                                                                                                                      MEDLINE=20287530; PubMed=10747866; Raian S., Wischmeyer E., Liu G.X.,
                                                                                                                                                                                 TISSUE-BRAIN;
                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                             POTASSIUM CHANNEL
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Vega-Saenz de Miera E.C., Lau D.H.P.,
Coetzee W., Rudy B.,
"KT3.2 and KT3.3 Two Novel Human Two I
                                                                                                                         "TASK-3, a novel tandem proe domain acid-sen actracellular histidine as nH sensor ":
                                                                                                                                                                                                                 NCBI_TaxID=10141;
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SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTF1; :- ACVNSTELDELIQQIVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                             AVAFSHFEGWTFFHAYYYCFITLTTIGFGDFVALQSG-E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIF',
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                                                                                                                                                                                                                              Rodentia;
                                                                                                                                                     E., Liu
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Last annotation update)
                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 351.5;
Pred. No. 5.
                                                                                                                                                                                                                             Craniata; Verrebrata; Euteleostomi;
Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                      PRT;
261DC973FF55AF91 CRC64;
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Query Match
Best Local Similarity
Matches 94; Conser

Conservative

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Score 351.5; Pred. No. 5.9e 59; Mismatches

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Best Local Similarity
Matches 90; Conserv
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Submitted (SEP-1997) to the EMBL; AF022821; AAD09338.1;
InterPro; IPR000099; -.
InterPro; IPR001622; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY 2000 (TrEMBLrel 13, Created)
01-MAY 2000 (TrEMBLrel 13, Last sequence update)
01-MAR-2000 (TrEMBLrel 16, Last annotation update)
01-MAR-2001 (TrEMBLRel 16, Last annotation update)
PUTATIVE POTASSIUM CHANNEL DP4 (FRAGMENT).
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; ZPOREKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gan L., Joiner W.J.,
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                                                                                                                              LIQQIVAAI---NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIF 158
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CMFYALLGIPLTLVMFQSLGERI-----
                                               CIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTK-----IRII
                                                                                                   ELERVVLRLKPHKAGV
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299 AA;
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33325 MW; DCD41D8A212939C4 CRC64;
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                                                                                                                                                                                                                                                                                                                           16.5%; Score 344; DB 11; 30.7%; Pred. No. 1.6e-17;
                                                                                                                                                                                                                                                                                                         61,
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                                                                                                   QWRFAGSFYFAITVITTIGYGHAAPSTDGGKVF
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  -NTFVRYLLHRAKRGLGMRHAEVSMA
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  155
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Best Local
                                                                                                     O76795 PRELIMINARY; PRT; 329 A.: O76795; O1-NOV-1998 (TrEMBLrel. 08, Created) O1-NOV-1998 (TrEMBLrel. 08, Last sequence to compare the potastive potassium Channel Subunit N2P38.
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SEQUENCE FROM N.A. Wang Z.-W., Salkoff L.; "Potassium channels in C. Submitted (AUG-1998) to t
                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2000) to the EMBL/GenBank/DDN: ....bases EMBL; AL118522; CAC14068.1; - SEQUENCE 330 AA; 36222 MW; 24F428721A1C7 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Primates; Catarrhini; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DJ781B1.1
                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                       AVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSD
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                                                                                                                                                                                                                                                                                                                                             PLEGELLAGVGDQLGTIEGKGIAKVEDTE-IKWNVSQT
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90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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C. elegans.";
the EMBL/Gen
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 EMBL/GenBank/DDel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 343.5; DF
Pred. No. 2e-17:
4; Mismatches
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  databases
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Homo.
                                                                                   Rhabditoidea;
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AF083652; AAC32863.1;

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Best Local S
Matches 94
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01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9NPC2;
                                                                                                                                                                                                                                                                                                              MEDLINE-20287530; PubMed-10747866; MEDLINE-20287530; PubMed-10747866; MEDLINE-20287530; PubMed-10747866;
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                      Girard C., Lesage F., Tinel N., Lazdunski M.; "Human Task-3, a novel 2P domain potassium channel related Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCNK9.
Homo sapiens (Human).
Tharvota; Metazoa; Chordata; (
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InterPro;
                                  SEQUENCE FROM N. TISSUE-BRAIN;
                                                                                                                                                                                                                                     Karschin A., Derst C.;
"TASK-3, a novel tandem proe domain acid-sensitive
extracellular histidine as pH sensor.";
J. Biol. Chem. 275:16650-16657(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2000 (TrembLrel. 15,
01-MAR-2001 (TrembLrel. 16,
2P DOMAIN POTASSIUM CHANNEL
POTASSIUM CHANNEL KT3.2) (2F
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                                                                                                                                                                             SEQUENCE FROM N.A.
Vega-Saenz de Miera
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               PubMed=11042359;
                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GC-VLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVA---GGS---DIEYLDFY
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                                                                                                                                       e W., Rudy
and KT3.3
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IPR003280;
                                                                                              (APR-2000)
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                                                                                                                                       В.;
Two
                                                                                                                                                                           E.C.,
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34.1%;
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16,
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16, Last annotation update)
NEL TASK-3 (POTASSIUM CHANNEL TASK3)
(2P DOMAIN POTASSIUM CHANNEL).
                                                                                                                                                                             Lau
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                                                                                                                                       Human
                                                                                                EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                             D.H.P.,
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                                                                                                                                       Two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  343; DB 5;
No. 2.1e-17;
                                                                                                                                                                                                                                                                                                                     Preisig-Mueller
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DR EMBL; AF279809; AAF85982.1; -...
DR EMBL; AF212829; AAF63708.1; -...
DR EMBL; AF257080; AAG33126.1; -...
DR EMBL; AF248241; AAG31730.1; -...
DR InterPro; IPR000099; -...
Therefor: IPR003092; -...
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Best Local
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Q9H592;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DJ137F1.1 (NOVEL MEMBER OF THE POTASSIUM CHANNEL SUBFAMILY
SEQUENCE FROM N.A. Williams S.; Submitted (SEP-2000) to the EMBL; ALI36087; CAC07335.1; Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02034; TWIK_channel; 1
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
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Primates;
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26.5%;
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Pred. No. 2.7e-7;
8; Mismatches 147;
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 16.2%; Score 338; DB 11; Length 313; Best Local Similarity 31.8%; Pred. No. 4.7e-17; Matches 76; Conservative 48; Mismatches 107; Indels
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SEQUENCE
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
2P DOMAIN K+ CHANNEL TWIK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "TWIK-2, an inactivating 2P domain K+ channel.";
J. Biol. Chem. 275:28722-28730(2000).
EMBL; AF281304; AAG10508.1; -.
Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-SPRAGUE-DAWLEY;
MEDLINE-20435832; PubMed-10887187;
Patel A.J., Maingret F., Magnone V., Fosset M., Lazdunski
Honore E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9ERU5;
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                                                                                                                                                                                                                                                                140 GIPLNLVVL----NRLGHLMQQGVNHWASRLGGT---WQ-DPDKARWLAGSGALLSGLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 IVAAINAGIIPUGNSSNQVSHWDIGSSFFFFAGTVITTIGFGNISPRTEGGKIFCIIYALL 165
                                      233 I-EGWSALDAIYFVVITLTTIGFGDYVAGGSDIE-YLDFYKPVVWFWILVGLAYFAAVL 289
                                                                                                                                     137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 GIPLFGFLLAGVGDQLGTIFGKGI----AKVEDTFIKWNVSQTKIRIISTIIFILFGCVL 221
195 LEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRSLYKVLVTAYLFLGLVAMVLVL 253
                                                                                                                                                                               173 LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIFKH 232
                                                                                                                                                                                                                                                                                                                                                                                                                                         57 YLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIP 116 | | : | | : | | : ::::| | |
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                                                                                                                                                                                                                                                                                                                                                                                                      17 YLALGALLVARLERPHEARLRAELGTLREQLLRHSPCVAAHALDAFVERVLAAGRLGRAV 76
                                                                                                                                     LLTASAQRLSLLLTH--APLSWLSLRWGWHPQRAARWHLVALLMVIVAIFFLIPAAVFAY 194
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25344 MW; 7AB9FB847F242ECE CRC64;
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Search completed: August 28, 2001, 17:12:46

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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2042
1 MKRQNVRTLALIVCTFTYLL.....STGLHSLSTFRGLMKRRSSV 394
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Copyright (c) 1993 - 2000 Compugen
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DEX	DX	8.5	ID	RESULT																														
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Human potassium channel TASK1.	29-AUG-2000	AAY79674;	674 AAY79674 St	1		131.5	141	141	141	147 5	151	151	151	156	176.5	190.5	212.5	245.5	253	278.5	294.5	295.5	295.5	295.5	295.5	319	319	320.5	320.5	326.5	3 6 6 6	363		
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			394 AA.		ALIGNMENTS	AAY34123	AAG41829 .	AAG41831	AAB40248	AAG40369	AAG14159	AAG40370	AAG14160	AAY79676	AAY28498	AAY79677	AAB31800	AAB31801 AAR97984	AAR97986	AAB31799	AAY90354	AAY68737	AAY90355	AAY25116	AAY34132	AAY / 96 / 5	AAY90356	AAY79673	AAW23397	AAY30647	AAY 94425	AAB50044		
÷~•		-		•	VTS											•						-					₹.					-	T+ 14	 -
						CO.	Arabidopsis thalia		Human ORFX ORF12 p	Arabidopsis thalla			Arabidopsis thalia	Caenorhabditis ele	Partial h-TREK1 po	Caenorhabditis ele	Amino acid sequenc	Amino acid sequenc	F22b7.7 potassium	Amino acid sequenc	Human TWIK-3 prote	KT4, a TWIK tamily	Human TWIK-4 prote	hTREK-1 pro	Human potassium ch			otassi	TWIK-1 potassium c	A mechanically sen	h-TRAAK	TREK. I		

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18-MAY-2000.
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                                                                           Modified-site
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323
                                                                           Location/Qualifiers
                               /note=
393
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                                               /note-
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                           'note=
                                    "O-phosphorylated"
                                                          "O-phosphorylated"
                                                                     "N-glycosylated"
                          "O-phosphorylated"
                                               "O-phosphorylated"
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TASKI: TWIK-related acid-sensitive K+ channon potassium channel; drug screening; hypertens hypotensive; epilepsy; arrhythmia; vascular neurodegenerative disease; ischaemia; anoxia; muscle disease;

human;

indocrine disease;

disease; therapy.

polypeptid

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of human TASK1 (TWIK-related acid-sensitive K+ channel), a member of a new family of 2P domain potassium channels, also including TWIK-1 (see AAY79673) and novel TASK2 (see AAY79675). TASK1 is expressed in many different tissues, and at particularly high levels in pancreas and placenta. Host cells expressing TWIK-1 family members can be used to screen for substances that modulate the activity of members of the TWIK-1 family of potassium channels. The drugs identified may be useful in the treatment of diseases of the heart or of the nervous system, such as epilepsy, arrhythmia, vascular diseases, neurodegenerative diseases, kidney, liver or pancreas diseases, hypertension, diseases associated with anomalies of hormone secretion, and muscle diseases associated with anomalies of hormone secretion,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding a non-inactivating outwardly rectifying potassium transport channel, designated TASK2, useful in the treatment of hypertension or dysfunctions of the kidney, liver or pancreas -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-1998;
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CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV
                                                                                                    YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
                                                                                                                                                                                                                       TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH
                                                                                                                               LVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGGGGGAHTTDTASSTAAAGGGGFRNVY
                                                                                                                                                                                                             tlvmfqslgerintlvryllhrakkglgmrradvsmanmvligffscistlcigaaafsh
                                                                                                                                                        yehwtffqayyycfitlttigfgdyvalqkdqalqtqpqyvafsfvyiltgltvigafln
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99US-0436265
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  394
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RESULT
AAY87291
ID AAY8

AAY87291

standard;

Protein;

394

Query Match

100.0%;

Score 2042;

DB

21;

Length

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26-JUN-1998;
31-JUL-1998;
01-OCT-1998;
                                                                                                                                                                                             reproductive or developmental disorders, (e.g. arteriosclerosis, clirhosis, psoriasis, acquired immune deficirry syndrome, anaemia, asthma, Crohn's disease, microbial or other protions, congestive or ischaemic heart disease, Alzheimer's, Parking sor Huntington's diseases, schizophrenia, ovulatory defects, rescular dystrophy). HSPP nucleic acids can be used for the recombinant conduction of HSPP, for detecting HSPP in standard hybridisation and implification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen ior agonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; signal peptide-containing protein; HSL. 31 diagnosis; cancer; inflammation; cardiovascular disease; antic; anti-inflammatory; antimicrobial; nootropic; neuroprotective; car. ovascular; hepatotropic, antiasthmatic; gene therapy; cell proliferation; neurological disorder; reproductive disorder; developmental disorder; arteriosclerosis; clirhosis; psoriasis; acquired immune deficiency syndrome; anaemia; asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia; parkinson's disease; Huntington's diseases; ovariatory defect;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSPP are used to treat or prevent disorders :-sociated with increased activity or function of HSPP. Such diseases :-clude cell proliferation (including cancer), inflammation, cardiovascular, neurological,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human signal peptide-containing proteins HSPI to HSPP-134. HSPPs have anticancer, anti-inflammatory, antimicrobial cotropic, hepatotropic, neuroprotective, cardiovascular and antiast) to activities, and can be used in gene therapy. HSPPs can be used to reevent disorders associated with decreased activity or function of HSPP. Antagonists of associated with decreased activity or function of HSPP. Antagonists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflemmation and cardiovascular disease -
                                                                                                                                    monitor, HSPP-related
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Sequence
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hypotensive; epilepsy; arrhythmia; vascular diseases;
neurodegenerative disease; ischaemia; anoxia; endocrine
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08-NOV-1999;
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Matches 357;
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22-JAN-2001 (first entry)

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Amino acid sequence of a human DKCN1 polype)

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Human; DKCN1; potassium channel; cancer; potasse; depring cardiovascular disease; inflammatory disease; pail we cardiovascular disease; schizophrenia; neurod; in erative disease; pail we psychiatric disorder; schizophrenia; neurod; in erative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding a non-inactivating potassium transport channel, designated TAS% of hypertension or dysfunctions of the kidne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and muscle diseases.
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                                                                                                                                                                                                               mfqslgerintfvryllhrakrglgmrhaevsmanmvliu1vscistlcigaaafsyyer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSIDSGKVFCMFYALLGIPLTLV 123
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88.1%;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's disease; neurological disorder; migraine; epilepsy; sleep-related disorder; erectile dysfunction; alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis and treatment of cancer, inflammatory and renal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides and polynucleotides of the potassium channel family, useful for identifying agonists/antagonists of therapeutic use and diagnosis and treatment of cancer, pulmonary, cardiovascular,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-1999; 99GB-0005061.
10-FEB-2000; 2000GB-0003112.
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                                                                                                                                                                             TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
                                                           kadvpdlqsvcsctcyrsqd--
                                                                                       -AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSR 359
                                                                                                                LVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGGGGGGAHTTDTASSTAAAGGGGFRNVY
                                                                                                                                                                                                              YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGAFLN
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Pred. No. 4.2e-113;
4; Mismatches 96;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptides and polynucleotides of the potassium channel family, useful for identifying agonists/antagonists of herapeutic use an diagnosis and treatment of cancer, pulmonary, ordiovascular,
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psychiatric disorder; schizophrenia; neuroded merative disease;
Alzheimer's disease; neurological disorder; r'uraine; epilepsy;
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                                                                                                                                                                                                       TLYMFQSLGERINTLYRYLLHRAKKGLGMRRADVSMANNVL; FFSCISTLCIGAAAFSH 180
                                                                                                    2000-587424/55.
DB; AAA75887.
tlvmfqslgermntfvryllkrikkccgmrntdvsmenmvtv4ffscmgtlcigaaafsq
                                                                                                                                                        ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page
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                                                                                                                                                                                                                                                                                                                                         54.7%; Score 1116; DF (1; 59.0%; Pred. No. 4.2e-13;
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                                                                                                                                                                                                                                                                                                              44;
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The present sequence represents tandem pore domain weak inward potassium (K+) (TWIK) polypeptide. The specification describes TWIK2, TWIK3, TWIK4, TWIK5, TWIK6, TWIK7, and TWIK1. The TWIK channel nucleic acids and proteins are used in screening assays to identify candidate compounds which are potential pesticides or therapeutics. The TWIK channel nucleic
                                                               New tandem pore domain weak inward rectifying potassium ion (TWIK) channel nucleic acids and proteins, useful in assays for identifyi candidate compounds which are potential pesticides or therapeutics
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                                                 Claim
                                                                                                 N-PSDB;
                                                                                                                                 Francis-Lang HL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVVLRFMTMNAEDEKRDAEHRALLTRNGQAGGGGGGSAHTTDTASSTAAAGGGGFRNVY
                                                5; Page 83-85; 96pp; English
                                                                                                                                                                                                                                                                                                                                                                 TWIKS;
                                                                                                 AAF25380
                                                                                                                        Gendreau SB,
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5; TWIK6; TWIK7; TWIK1; pesticide; ion
                                                                                                                                                                                                                                                                                                                                                                                                         (first
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161..177
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184..207
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224..24
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SB, Jacobus
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DA, Tietjen K,
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Jeschke P;
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in living cells that can be used to study t
regulation, and their use as pesticide or or
                                                                                                                                                                                                                                                                                             AAB31805 standard; Protein;
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5; TWIK6; TWIK7; TWIK1; pesticic
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Pred. No. 1.30
6; Mismatches
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/note= "t 235..259

"pore

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          TWIK2; TWIK3;
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Best Local Similarity
Matches 110; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which are potential pesticides or therapeutics. The TWIK channel nucleic acids can be used for generating mutant phenotypes in animal models or in living cells that can be used to study the ion channels, their regulation, and their use as pesticide or drug targets, and as hybridisation probes and replication/amplification primers. TWIK channel proteins are useful as immunogens to generate monoclonal or polycional antibodies, and in assays to identify molecules that would specifically bind to them. Genetically engineered metazoan invertebrate animals may be used in studying TWIK channel activity, and for screening and identifying new drug targets, therapeutic agents, diagnostics and prognosis useful in treating disorders associated with ion channels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (K+) (TWIK) polypeptide. The specification describes TWIK2, TWIK3, TWIK5, TWIK6, TWIK7, and TWIK1. The TWIK channel nucleic acids and proteins are used in screening assays to identify candidate compounds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tandem pore domain weak inward rectifying potassium ion (TWIK) channel nucleic acids and proteins, useful in assays for identifying candidate compounds which are potential pesticides or therapeutics -
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glqygagfsphned
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                               G---GGGGSAHTTDTASSTAAAGGGGFRNVYAEVLHFQS 308
                                                                kimttcylflgitim--mltltvfydipqlnlgllfttsedsek--
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SB, Jacobus DA, Tietjen
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                                                                                                                                                                                                                                                                                             channel protein designated TREK-1. The protein is activated by polyunsaturated fatty acids, particularly at indonce acid, and by riluzole. The protein is used to screen for soft the heart and nervous systems in humans and animals, e.g. epilepsy indiovascular disease (arrhythmia), neurodegeneration (particular), increasing disease. The protein itself may be used to the cretion and muscular disease. The protein itself may be used to the these diseases. Antibodies specific for the protein are used.
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system disorders
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                                                                     FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKG
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                          ANMVLIGEFSCISTLCIGAAAFSHYEHWTFFQAYYYCFI". TTIGFGDYVALQKDQALQT 216
                                                                                                                                                          mkwktvstiflvv--vlyliigaavfkaleqpqeisqr
                                                   fciiyallgiplfgfllagvgdqlgtif---
                                                                                                                                                                                                                93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ē
                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fink M,
                                                                                                                                                                                                                                                                                  370 AA;
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98FR-0002725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-FR00404
                                                                                                                                                                                                                            18.1%;
31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lazdunski M,
                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          370 AA
                                                                                                                                                                                                                           Score 369; DB
                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lesage
                                                                                                                                                                         <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F. € D.⊃rat
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                                                              RAD-----VSM 156
                                                    akvedtfikwnvsqtkiri
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                                                                                                                                                           :iqkqtfiaqhacvns--t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eed to screen for
as for heart and nervous
                                                                                                                                                                                                                                       Length 370;
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                42;
                                                                                                                                                                                                               Gaps
                                                    208
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QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTRN

267

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RESULT
AAY28497
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                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                  This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1 polynucleotide AAZ00040. h-TREK1 is a two pore potassium channel. The polynucleotide sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptides. The methods of diagnosis may be used in the
                                                                                                                                                                                                                                                                                                            treatment of diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative diseases including Alzheimer's,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New two pore potassium channel used for, e.g. treapulmonary, cardiovascular and inflammatory diseases {\sf pulmonary}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-OCT-1998;
27-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h-TREK1; two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY28497 standard;
                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                             stroke, and head trauma and neurological disorders including migraine.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-469126/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9937762-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse h-TREK1 polypeptide.
  157
                              158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 ldfykpvvwfwilvglayfaavlsmigdwlrviskktkeevgefrahaaewtan 320
                                                        109
                                                                                    98
                                                                                                              61
                                                                                                                                          42
                                                                                                                                                                    1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
ANMVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT
                                                                                                             ELERVVLRL-KPHKAGV------QWRFAGSFYFAITVITTIGYGHAAPSTDGGKV 108
                                                                                                                                       mkwktvstiflvv--vlyliigaavfkaleqpqeisqrttiviqkqtfiaqhacvns--t
                    ||: ||||||| : :|:::|:
|fcilyallgiplfgfllagvgdqlgtif-----gkgiakvedtfikwnvsqtkiri 208
                                                       FCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRAD------VSM 156
                                                                                eldeliqqivaainagiiplgnssnqvshwdlgssfffagtvittigfgnisprteggki 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMITHKLINE BEECHAM PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1q32.
                                                                                                                                                                                                                                                                     411 AA;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Meadows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pore potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                      26; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98GB-0022135
98EP-0300570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                            18.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    된
                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            411 AA
                                                                                                                                                                                             Score 369; DB 20;
Pred. No. 1.5e-31;
7; Mismatches 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammatory
                                                                                                                                                                                                102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treatment of
                                                                                                                                                                                                                         Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease;
                                                                                                                                                                                                Indels
                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer
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  216
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RESULT 10
AAY34133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JAN-1999;
25-FEB-1998;
07-AUG-1998;
                                                                                                                                               disorders. Nucleotides encoding K+Hnov proteins may be used for identifying homologous or related proteins at the DNA sequences encoding them. They may be used to produce compositions that modulate the expression and function of the K+Hnov prote; and in studying the biochemical pathways associated with it. They, may also be used for the
                                                                                                                                                                                                                                                                                                  polymorphisms detected as sequence variants by ween multiple independent clones. Potassium channels have controlled in roles in various cell types and biochemical pathways. Defective potassium channels are known to cause four human diseases: episodic a axia with myokymia; cardiac arrhythmia (long OT syndrome); epilepsy; and Bartter's syndrome. As potassium channels are critical component. If virtually all cells, it is likely that abnormal potassium channed are also implicated in certain renal, cardiovascular and central network system (CNS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wills sequence represent the form of homology to known potassium k+Hnov proteins have a high degree of homology to known potassium channel, channels and may be alpha subunits, which for the functional channel, or accessory subunits that act to modulate the channel activity. K+Hnov59 or accessory subunits that act to modulate the channel activity. K+Hnov59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is a 4 transmembrane domain, 2 pore domain. ....ssium channel. is located on chromosome 19, determined via. .....chromosomal localisation using primers AAZI1939 and AAZI1 0. KHHnov cDNAs were isolated by extension of expressed segue e tags (ESTs) where the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acids encoding mammalian K+Hnov ...assium channel proteins, useful for the diagnosis and tree of episodic with myokymia, cardiac arrhythmia, epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-527591/44.
N-PSDB; AAZ11915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the human K+Hnov5'7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Page 104-105; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curran ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-SEP-1999.
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Potassium channel; ataxia; arrhythmia; epi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-NOV-1999
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                                                          additionally, such nucleotides may be used . the treatment of diseases associated with a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AXYS-) AXYS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular
                                                                                                                     recombinant production of K+Hnov protein in termination cultures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ldfykpvvwfwilvglayfaavlsmigdwlrviskktkooveefrahaaewtan 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
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98US-0076687.
98US-0095836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US03826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ξ
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                                                       hene therapy protocols for all potassium channels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assium channel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              order.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                   polynucleotide AAZ00039. h-TREK1 is a two pore potassium channel, and the gene maps to human chromosome 1q32, between the markers D1S237 and WI5105. The polynucleotide sequence of h-TREK1 can be used to diagnose a disease or susceptibility to a disease related to expression or activity of h-TREK-1 polypeptides. The methods of diagnosis may be used in the treatment of diseases including cancer, pulmonary, cardiovascular, and inflammatory diseases, pain, psychiatric disorders including depression and schizophrenia, neurodegenerative diseases including Alzheimer's,
            stroke,
                                                                                                                                                          Claim 3;
                                                                                                                             This sequence is the h-TREK1 polypeptide, encoded by the
                                                                                                                                                                                                                                                                Chapman CG,
                                                                                                                                                                                                                                                                                                                    09-OCT-1998;
27-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                          02-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                               WO9937762-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h-TREK1; two pore potassium channel; inflammatory disease;
chromosome 1q32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h-TREK1 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY28496 standard;
                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
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           trauma and neurological disorders including migraine
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31.0%;
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Pred. No. 7e-31;
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Claim 7;

Page

29;

35pp;

English

Huntington's chorea

The present sequence is human TREKI (h-TREK: h-iREKI is a member of the 2P domain potassium channel family of prote. which play a part in the control of resting membrane potential. Modulism on of these channels will therefore affect neuronal excitability, the leading to a modulation

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AAB50044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; TREK; 2P domain potassium channel; http://greenmountain.com/meuronal excitability; neurotransmitter re_b modulation; epilepsy; neurological disorder; sleep-related disorder by contine dysfunction; attention deficit disorder; addiction; anxive; phobia; Parkinson's chorea; Huntington's chorea; ce_vial palsy; incontinence
Use of human TREK1 polypeptide, polynucleoties encoding them and modulators of h-TREK1 polypeptides for treated polypeptides for treated polypeptides for treated polynucleoties, addiction and dyskinesias include parkinson's and the polynucleoties and the polynucleoties and polynucleoties.
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N-PSDB; AAC90412.
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RESULT 1
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Best Local S
Matches 91
           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurological conditions such as epilepsy, sleep-related disorders, cognitive dysfunction, attention deficit disorder, addiction, anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy, incontinence, erectile dysfunction or alopecia.
                                 Novel isolated h-TRAAK polypeptides belonging to the potassium channel family of polypeptides, useful for the diagnosis and treatment of h-TRAAK related disorders,e.g. depression and schizophrenia -
                                                                                                                                                                                                                                                                                                                                     2P domain potassium channel; neurodegenerative disease; st.
psychiatric disorder; neurological disorder; Gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of neurotransmitter release and activity of neuronal networks. Such modulation therefore may be useful for the treatment of certain
                                                                                                                                   Chapman CG,
                                                                                                                                                                                        03-NOV-1998;
07-OCT-1999;
                                                                                                                                                                                                                              03-NOV-1999;
                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                  Human; h-TRAAK; potassium channel polypeptide;
                                                                                                                                                                                                                                                                                                                                                                                              Human h-TRAAK polypeptide #1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY94425 standard;
                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM PLC
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         3; Page 21; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                   Duckworth
                                                                                                                                                                                        98GB-0024048.
99GB-0023668.
                                                                                                                                                                                                                                99WO-GB03634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
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31.0%;
                                                                                                                                   DM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393
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Pred. No. 7e-31;
9; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                     neurodegenerative disease; stroke;
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AAY94426
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Chapman CG,
                                                                                                                                                                                                                                                                                                                                                                          Human; h-TRAAK; potassium channel polypeptio;
2P domain potassium channel; neurodegenerat; disease; stroke; psychiatric disorder; neurological disorder; ne therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-AUG-2000 (first entry)
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                                                                                                                                                                                                                                   11-MAY-2000
                                                                                                                                                                                                                                                                                      WO200026253-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human h-TRAAK polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY94426 standard; Protein; 393 AA.
                                                (SMIK ) SMITHKLINE BEECHAM PLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98;
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31.0%;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                    Mechanically sensitive potassium channel protein; TRAAK; polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease; nervous system disease; epilepsy; cardiovascular disease; arrhythmia; neurodegeneration; ischemia; anoxia; hormone secretion abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        schizophrenia, neurodegenerative disease including Alzheimer's, s and head trauma and neurological disorders including migraine and epilepsy. The present sequence is human h-TRAAK protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Functional genomics was used to identify h-TRAAK polypeptides and h-TRAAK polypucieotides from human tissue samples. h-TRAAK polypeptides have homology to the 2P domain potassium channel family of polypeptides. The h-TRAAK polypeptides and polynucleotides may be used in diagnostic assays for conditions related to h-TRAAK imbalance and for identifying agonists and antagonists of h-TRAAK polypeptides. The h-TRAAK polypeptides and polynucleotides may also be useful for treatment and prevention (e.g. as vaccines) of certain diseases, such as pain, psychiatric disorders including depression and chiscabers, such as pain, psychiatric disorders including depression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; Pages 21 and 22; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated h-TRAAK polypeptides belonging to the potassium chafamily of polypeptides, useful for the diagnosis and treatment of h-TRAAK related disorders, e.g. depression and schizophrenia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-365583/31.
N-PSDB; AAA27106.
                                                       muscular
                                                                                                                                                                                                    18-NOV-1999
                                                                                                                                                                                                                                                                             AAY30647 standard;
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                                                                                                                                                            mechanically sensitive potassium channel protein TRAAK
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Matches 85
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30 84 4.1 1239 2 US-08-39-39-2: Sequence 32 881 4.0 553 4 US-09-385-59-2: Sequence 33 881 4.0 553 4 US-09-885-352-2: Sequence 33 881 4.0 553 4 US-09-083-351-2: Sequence 33 881 4.0 553 4 US-09-083-351-2: Sequence 35 880 3.9 242 2 US-08-553-497A-2: Sequence 36 880 3.9 242 2 US-08-553-497A-2: Sequence 37 880 3.9 488 1 US-08-553-497A-2: Sequence 38 880 3.9 488 1 US-08-553-497A-2: Sequence 38 880 3.9 488 1 US-08-553-497A-2: Sequence 38 880 3.9 488 1 US-08-553-497A-2: Sequence 39 79.5 3.9 887 270 2 US-08-820-170A-2: Sequence 40 79.5 3.9 887 270 2 US-08-820-170A-2: Sequence 41 79.5 3.9 887 4 US-09-273-565-28 Sequence 42 79.5 3.9 829 2 US-08-820-170A-2: Sequence 44 79.5 3.9 829 2 US-08-820-170A-2: Sequence 44 79.5 3.9 829 2 US-08-820-170A-2: Sequence 44 79.5 3.9 829 2 US-08-820-170A-2: Sequence 44 79.5 3.9 829 2 US-08-820-170A-2: Sequence 44 79.5 3.9 829 2 US-08-820-170A-2: Sequence 44 79.5 3.9 829 2 US-08-820-170A-2: Sequence 44 79.5 3.9 829 2 US-08-820-170A-2: Sequence 44 79.5 3.9 829 2 US-08-820-170A-2: Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 44 79.5 3.9 829 4 US-09-273-565-31 Sequence 50 40.0

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; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-2
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Best Local Similarity
Whethes 91; Conserv
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US-08-749-816-2
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CURRENT FILLING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Conrad Chapman
TITLE OF INVENTION: NO. 6242217el Compounds
FILE REFERENCE: GP30031
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                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                CLASSIFICATION:
                                   APPLICATION NUMBER: FILING DATE: 15-NO
                                                                                                                                                                                            COUNTRY:
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Barhanin, Jacques
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Lazdunki, Michel
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                                                                                                    E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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INFORMATION:
                                 15-NOV-1996
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Best Local Similarity 32.4
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versior
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION: TELEPHONE: 201-831-3246
                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REGISTRATION NUMBER:
                                                                      REGISTRATION NUMBER: .P-38,711 REFERENCE/DOCKET NUMBER: 32,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US . ZIP: 07470-8426
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                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                        Harrington, James J.
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Pausch, Mark H.
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INFORMATION FOR SEQ ID NO:

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; MOLECULE TYPE: protein US-08-332-312-2
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                                                                                                    TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Harrington, James
REGISTRATION NUMBER: P-3
                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Price, Laura A. APPLICANT: Pausch, Mark H. TITLE OF INVENTION: Melana
                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 LAILIVY-----TAFGGVLMSKLEPWSFFTSFYWSFITMTTVGFGDLMP-RRD----- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               158 NMVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 GERI-----MTL-VRYLL---HRAKK------GLG-----MRRADVSMA 157
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                                TOPOLOGY:
                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Wayne
                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                LENGTH:
                                                                                                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGKFLSEHLVWLYGNYLKLKYLILSRHRKERREHVCEHCHSHGMGHDMNIEEKRIPAFLV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
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                                               : 618 amino acids amino acid
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                                                                                                                                                                      32,421
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Pred. No. 9.1e-20;
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                                                                                                                                                                                                                                                                                                             Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 215-875-8383
                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
TITLE OF INVENTION: OF DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 SMANMVLIGEFSCISTL-CIGAAAFSHYEHWTFFQAYYYCFITUTTIGFGDYV-ALQKDQ 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 KVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKK---
                                                                                                                                                                                                                                                                                                                                            STREET: 230 CONTY: Philadelphia
                                                                                  NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
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                                 TELEFAX:
                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 15-NOV-1996
                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRSNSCPDLSMYRVEPAP-----IPSRKRAFSVCADMVGAQREA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKEFGGWFVVYQIFVIVWFIFSLGYL - - VMIMTFITRGL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RMIMIAYSVIGIPVNGILFAGLGEYFGRTFEAIYRRYKKYKMSTDMHYVPPQLGL----I 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ERVVLRL-----KP-----HKAGVQWRFAGSFYFAIIVITTIGYGHAAPSTDGG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWILLLIFYISYLMFGAAIYYHIEHGEEKIS-----RAEQRKAQIAINEYLLEELGDKN
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230 South Fifteenth Street, Suite 5:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Romey, Georges
Barhanin, Jacques
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                                   215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duprat, Fabrice
Lazdunki, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fink, Michel
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                                                                                                                                                                                                                                                                        Floppy disk
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                 ID NO:
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; STRANDEDNESS:
; TOPOLOGY: lin
; MOLECULE TYPE:
US-08-749-816-4
                                                                                                 US-08-749-816-3
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US-09-236-080-4
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Sequence 3, Application US/08749816
Patent NO. 6013470
GENERAL INFORMATION:
APPLICANT: Lesage, Florian
APPLICANT: Guillemare, Eric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/236,080
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEO ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 107
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Helen Meadows
APPLICANT: Conrad Chapman
                                                                                                                                                                                                                                                                                                                                 Query Match 8.6%; Score 176.5; DB Best Local Similarity 33.0%; Pred. No. 5e-12; Matches 34; Conservative 22; Mismatches
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Best Local Similarity 24.0
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: No. 6242217el Compounds FILE REFERENCE: GP30031
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164
                                                                                                                                                                                                                 138 YLLHRAKKGLGMRRAD-------VSMANMVLIGFFSCI 168
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                                                                                                                                                                                                                                                        WDLGSSEFFAGTVITTIGFGNISPRTEGGKIFCIIVALLGIPLFGFLLAGVGDQLGTIF- 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANMV-------
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                                                                                                                                                                                                                                                                                            WRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLVMFQSLGERINTLVR 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MCLIAYALLGIPLTLVTMADTGKFAAQLV-----TRWFGDNNMAIPAAIFVCLLFAYP 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --RVVLRLK-PHKAGV------QWRFAGSFYFAITVITTIGYGHAAPSTDGGK 107
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amino acid
                                                                                                                                                                            -GKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCV 102
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-749-816-3
                                                                                                                                                   US-08-288-405A-10
                                                                                                                                                                  RESULT
                                                                                          Sequence 10, Application US/08288405A Patent No. 5559009
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 3:
                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Weiser, Gerard J. REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 98
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version.
                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE
TITLE OF INVENTION: OF DRUGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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ADDRESSEE: WEISER &
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                      APPLICANT:
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                                                                                                                                                                                                                          201 YLIFLSSLLLCSISLLSSSALFSSIENISYLSSVYFGIITMFLIGIGDIV
                                                                                                                                                                                                                                                                                                                                     114 ALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRADV :MAN-----
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                                                                                                                                                                                                                                                                                                 SLLMIPVFIAFKFEFGTFLAHFLVVVSNRTR--LAVKKAYYKLSQNPENAETPSNSLQHD
                                                                                                                                                                                                                                                            --MVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCF11LTTIGFGDYV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 RQNVNVVVCLSAAITLLVFNLIGAGIFYLAETQN---SSES; NENSEVSKCLHNLPIGG- 86
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230 South Fifteenth Street,
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                                      Chandy,
                                                     Kalman,
                                                                        Chandy,
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Kanianthara G.
Katalin
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George A.
Roo. 5559009el Voltago
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INVENTION:

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.Potassium Channel

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CORRESPONDENCE ADDRESS

OF SEQUENCES:

STREET:

San Francisco

Embarcadero Center, Suite 3400

Flehr, Hohbach, Test, Albritton & Herbert, Attn: Walter H. Dreger

ADDRESSEE:

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                     SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 626
TYPE: PRT
                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                Sequence 2, Applic
Patent No. 5986081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                           CURRENT APPLICATION NUMBER: US/08/956,242C CURRENT FILING DATE: 1997-10-22 NUMBER OF SEQ ID NOS: 13
                                                                                                                                                   APPLICANT: Ganetzky, Barry S. APPLICANT: Titus, Steven A. TITLE OF INVENTION: Polynucleotides Encoding Herg-3 FILE REFERENCE: 960296.94550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 532 amino acids
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08/207,431
                                                                                                                                                                                                                                                                                                                                                                                                                                           412 DRV----DTHFTSI----PESFWWAVVTWTTVGYGDMAPVTVGGKIVGSLCAIAGVLTIS 463
                                                                                                                                                                                                                                                                                                                                                                   464 LPVPVIV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      382 RASMRELGLLI---SFLFIGVVLFSS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 ERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGI---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 5.0%; Score 103; DB 1; Local Similarity 22.8%; Pred. No. 0.0085; ses 34; Conservative 27; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 04-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 RONVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYEEL 62
                                                                                                                                                                                                                                                                                                                                                                                                       -PLTLVMFQSLGERINTLVRYLLHRAKKG 146
                                                                                                                                                                                                                                                                      Application US/08956242C
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910 277299
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Dreger, Walter H.

Dreger, Walter H.

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LOCATION: (441)..(542)
COTHER INFORMATION: Unidentified at time of il. (19
US-08-956-242-2
US-08-464-340A-4
                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: unsure
; LOCATION: (441)..(542)
; OTHER INFORMATION: Uni
US-09-351-215-2
                    RESULT
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Best Local Similarity
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CURRENT FILING DATE: 1999-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ganetzky, Barry S.
APPLICANT: Titus, Steven A.
TITLE OF INVENTION: Polynucleotides Encoding
FILE REFERENCE: 960296.94550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1997-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 08/956,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                         121 TLVMFQSLGERINTLVRYL 139
                                                                         374 -SLMYASIFGNVSAIIQRL
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                                                                                                                                                                                                                     274 LFLLMCTFALIAHWLACIWYAIGN----VERPYLEHKIGW: OSLAVQLGKRYNGSD---- 325
                                                                                                                                                                                 61 ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAFSfDGGKVFCMFYALLGIPL 120
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23.7%;
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23.7%; Pred. No. 0.0
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Sequence 4, Application US/08464340A Patent No. 5710019

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PCT-US94-08449A-4
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                   Sequence 4, Application PC/TUS9408449A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 494 AMINO ACIDS
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APPLICATION NUMBER: PCT/US94/08449

FILING DATE: 28 JUL 1994

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 201-994-1700
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: PROTEIN
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REFERENCE/DOCKET NUMBER: 325800-415
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                                                                                                                                                                                                                                                                                                               ALGYTMEQSHPE--TLFKNIPQSFWWAIITMTTVGYGDIYPKTTLSKLNA------AI 389
                                                                                                                                                                                                                                                                                                                                                     AAAF----SHYEHWTFF----QAYYYCFITLTTIGFGDY---VALQKDQALQTQPQYVAF 223
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GENERAL INFORMATION:
                   Sequence 4, Application US/08956242C Patent No. 5986081
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Best Local :
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REGISTRATION NUMBER: 36,
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LENGTH: 494 AMINO ACID
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FILING DATE: SUBMITT
CLASSIFICATION:
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ALIVCTFTYLLY-GAAVFDALESEPEL----IERQRLELK, ELRARYNLSQG--GYEEL 62
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                                                                                                                                                                                                                                                                                                          ALGYTMEQSHPE--TLFKNIPQSFWWAIITMTTVGYGDIN, KTTLSKLNA-----AI
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NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 4
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APPLICANT: Titus, Steven A.
TITLE OF INVENTION: Polynucleotides Encoding
FILE REFERENCE: 960296.94550
CURRENT APPLICATION NUMBER: US/08/956,242C
CURRENT FILING DATE: 1997-10-22
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ORGANISM: Homo sapien
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LOCATION: (133)
OTHER INFORMATION: Unidentified at time
LOCATION: (610)
OTHER INFORMATION: Unidentified at
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LOCATION: (608)
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Sequence 4, Application US/09351215
Patent No. 6087488
GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-07-12
EARLIER APPLICATION NUMBER: 08/956,242
EARLIER FILING DATE: 1997-10-22
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APPLICANT: Titus, Steven A.
TITLE OF INVENTION: Polynucleotides Encoding Herg-3
FILE REFERENCE: 960296.94550
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SOFTWARE: PatentIn Ver.
NAME/KEY: unsure
LOCATION: (600)
OTHER INFORMATION: Unidentified at time of filing
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Query Match Matches

Local Similarity hes 31; Conserv

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Mismatches

45: Indels 49; Length 888;

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LOCATION: (637)
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LOCATION: (629)
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OTHER INFORMATION:
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OTHER INFORMATION:
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Db Oy	236 QQIGKRYNDSDSSSGPSIKDKYVTALYFTFSSLTSVGFGNVSPNTNS 282 106 GKVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKG 146 1:1:1:1:1:1:1:1:1:1 283 EKIFSICVMLIGSLMYASIFGNVSAIIQRLYSGTARYHMQMLRVKEFIRFHQIPNP 338 147 LGMRRADVSMANMVLIGFFSCI-STLCI 173 1
Qy	106 GKVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKG 146
Db	283 EKIFSICVMLIGSLMYASIFGNVSAIIQRLYSGTARYHMQMLRVKEFIRFHQIPNP 338
Qγ	147 LGMRRADVSMANMVLIGFESCI-STLCI 173
Db	339 LRQRLEEYFQHAWTYINGIDM-NWVLKGFPECLQADICL 376
Searc Job t	Search completed: August 28, 2001, 17:06:23 Job time: 527 sec

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Title: Perfect score: Sequence: OM protein - protein search, using sw model Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Total number of hits satisfying chosen parameters: Scoring table: Run on: Searched: US-09-503-089A-5
2042
1 MKRQNVRTLALIVCTFTYLL....STGLHSLSTFRGLMKRRSSV 394 August 28, 2001, 17:07:05; Search time 36.66 Seconds (without alignments) 818.679 Million cell updates/sec BLOSUM62 Gapop 10.0 , Gapext 0.5 219241 seqs, 76174552 residues GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. 219241

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	N	1	No.	Result	
	229	231.5	•		235.5	•	243	244	245	247.5	248	250	251	251	256.5	258	258.5	259.5	261.5	262	268	275	293	307.5	320.5	599	599	806.5	820	Score		
	11.2		11.3	11.5	11.5	11.7		11.9	12.0		12.1	12.2	12.3	12.3	12.6	12.6	12.7	12.7	12.8	12.8	13.1	13.5	14.3	15.1	15.7	29.3	29.3	39.5	40.2		Query	•
	325	519	484	485	475	522	528	381	769	392	444	569	576	544	452	383	427	335	1001	443	1539	524	393	513	336	364	334	336	329	Length [
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	T15584	T16629	T43529	T24201	T27725	T24265	T21834	T43393	T27550	T45032	T26229	T43531	T43363	T43364	T21118	T23182	T27681	S44635	T13807	T21598	T30037	T23907	T25392	T28933	S65566	T43361	T19860	T32347	T43509	ID		
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J 4	43	42	41	40	39	38	37	36	35	34	ω 3	32	31	30
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9.3 9.1	9.3	9.5	9.8	9.8	9.9	9.9	10.1	10.3	10.3	10.3	10.6	10.6	10.9	11.2
631 681	383	523	660	700	555	551	586	1136	504	539	643	350	600	461
NN	2	2	N	2	N	2	N	2	N	Ŋ	2	N	2	2
T26232 T19429	T23746	T23373	T21551	T27364	T43357	T16426	T21683	T26953	T22269	T23700	T26616	T15178	T24626	T43394
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ALIGNMENTS

Outward C;Specie C;Date: C;Access	RESULT		0γ	DЬ	Qy	рь	Qy	Db	Qy	Db	Qy	Db	Qy	Query Ma Best Loo Matches	A; Residues: A; Cross-ref	A;Stat A;Mole	A;Reie A;Acce	submit A; Desc	C; Date C; Acce	probable p	RESULT T43509
rectifler potassium channel homolog twk-2 ss: Caenorhabditis elegans 29-Oct-1999 #sequence_revision 29-Oct-1995 sion: T32347	2		295 GFRNVYAEVLHFOSMCSCLWYKSREKLOYSIPMIIPRDD FISHTCVEOSHSSPGGG 350	238 MNLLVLRFLTMNTEDERRDEQEAILAAQGLVRVGDPTAL DFGRLPLSDNVSLAS 292	239 LNLVVLRFMTMNAEDEKRDAEHRALLTRNGQAGG; GSAHTTDTASSTAAAGGG 294	178 SSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSLQ: YVFFSLVFILFGLTVISAA 237	179 SHYEHWTEFQAYYYCEITLTTIGFGDYVALQKDQALQT. ŞYVAFSFVYLLTGLTVIGAF 238	121 GLIMFQSIGERMNTFAAKLLRFIRRAAG-KQPIVTSSDI : FCTGWGGLLIFGGAFMF 177	121 TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANN 5,3 FFSCISTLCIGAAAF 178	61 ILEATIVKSVPHKAGYQWKFSGAFYFATTVITTIGYGH: "DAGKVFCMLYALAGIPL 120	61 ELERVYLRLKPHKAGYQWRFAGSFYFAITVITTIGYGH/ CTDGGKYFCMFYALLGIPL 120	1 MKRQNIRTLSLIVCTLTYLLVGAAVFDALETENEILORF # RVREKLKTKYNMSNADYE 60	1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIEK. + J.RQQELRARYNLSQGGYE 60	atch 40.2%; cal Similarity 48.3%; 172; Conservative 54	A;Residues: 1-329 <wan> A;Cross-references: EMBL:AF083652; PIDN:AAC32863</wan>	A;Status: preliminary; translated from GB/EMBL/DDT. A;Molecule type: mRNA	A; Reference number: 222450 A; Accession: T43509	submitted to the EMBL Data Library, August 1998 A;Description: Potassium channels in C. elegans.	n-2000 #sequence_revision 21-Jan-20 T43509	otassium «	⊒ Soveri

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R;Murray, J.; Wohldmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F34D6
A;Reference number: 221153
A;Recession: T32347
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-336 <MURP
A;Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GS
A;Experimental source: strain Bristol N2; clone F34D6
C;Genetics:
A;Gene: twk-23; CESP:F34D6.3
A;Map position: 2
A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 29
                                                                                                                                                                                                                                                                                        hypothetical protein C40C9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T19860
                                                                                                                                                                                                                                                                                                                                                          RESULT
T19860
                                                                            A; Gene: CESP:C40C9.1
A; Map position: X
A; Introns: 34/1; 60/2;
                                                                                                                              A; Experimental source: C; Genetics:
                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-334 <WIL>
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Best Local Similarity 47.4
Matches 172; Conservative
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Conservative
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               29.3%;
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46;
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Pred. No. 5.
               Score 599; DB 2; Pred. No. 5.1e-47;
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Mismatches
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81;
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12;
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Gaps
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RESULT
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A;Description: Potassium channels in
A;Reference number: 22450
A;Accession: T43361
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C; Date: 11-Jan-2000
C; Accession: T43361
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A; Residues: 1-364 <WAN>
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Best Local Similarity
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                                                                                                           AAFSHYEHWIFFQAYYYCFIILITIGFGDYVALQKDQALOK&QYVAFSFVYILIGLIVI
                                                                                                                                                                  MFQSLGERINTLYRYLLHRAKKGLGMR----RADVSMAN VI ----IGFFSCISTLCIGA 175
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                                                                                                                                            MFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTH LLAVSLTIGFMVIVS----GT
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n C. elegans.
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inward rectifier potassium channel TWIK-1 - human C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997
C;Accession: \$65566
R;Lesage, F; Guillemare, E; Fink, M; Duprat, F;
EMBO J. 15, 1004-1011, 1996
A;Title: TWIK-1, a ubiquitous human weakly inward x

human weakly inward rectifying K(+)

channel with a

G.;

Barhani nove

M.; Duprat, F.; Lazdunski, M.; Romey,

#rext_change 05-Nov-1999

wif

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C; Accessic
R; Nelson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
T28933
hypothetical protein C52B9.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: S65566; MUID:96183184
A;Accession: S65566
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-336 <LES>
A;Cross-references: EMBL:U33632; NID:g1086490;
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A; Introns: 12/3;
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                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U64598; PIDN:AAC47976.1; GSPDB:GN00028; CESP:C52B9 A;Experimental source: strain Bristol N2; clone C52B9
                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-513 <NEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description: The sequence A; Reference number: Z20545
                                                                                                                                                                                                                                                                                                                                A; Gene: CESP:C52B9.6
                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated
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Best Local
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Best Local Similarity
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                                                                                                                                                        VGLVILLFLYLIAGAFLFRYLEAPKELEDSDNRISREAFNAINQEY----
                                                                                          VKNMFQAYRNQFITAKHLLNKTREDEVLWTFPNSMFFAATVITTIVQVKNRSGNRVVFSR 172
                                                                                                                                                                                    LALIVCTFTYLLVGAAVFDALESEPEL-----IERQRLELRQQELRARYNLSQGGYEEL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAFSHYE-HWTFFQAYYYCFITLTTIGFGDYVA----LQKDQALQTQPQYVAFSFVYIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVMFQSLGERINTLVRYLLHRAKKGL-----GMRRADVSMANMVLIGFFSCISTLCIG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFT 145
                                                                                                              ERVVLRL------KPHKAGVQWRFAGSFYFAITVITTI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLFLTAVVQRIT-----VHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIP 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEA
                             GYGNLVPITVTGRVACIIFALLGIPLLLVTIADIGKFLSEFLSY-LYRSYRGFKRKLRRQ
                                                           GYGHAAPSTDGGKVFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGLIAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TG----LTVIGAFLNLVVL---RFMTMNAEDEKRDAEH
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                                                                                                                                                                                                                                                                                                   12/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T28933
                                                                                                                                                                                                                                                                                                   54/3;
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                 90/3; 158/1; 173/1; 227/3; 299/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -QWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLT 121
                                                                                                                                                                                                                                    15.1%;
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Pred. No. 1.5e-21;
                                                                                                                                                                                                                                    Score 307.5; D
Pred. No. 3.9e-
                                                                                                                                                                                                                                                                                                                                                                                                                              from GB/EMBL/DDBJ
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RADVSMANMVLIGEF 165
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                                                                                                                                                                                                                                                                                               346/2;
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                                                                                                                                                                                                                                                                                                 378/2;
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                             231
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hypothetical protein R04F11.4 - Caenorhabditis C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1 C;Accession: T23907 R;Harris, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T25392
A;Status: preliminary; translated from GB/EMBL/DLt3
A;Molecule type: DNA
A;Residues: 1-393 <WTI>A;Residues: 1-393 <WTI
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-199
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  submitted to the EMBL Data Library, June 1996
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Best Local S
Matches 78
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                                                                                                                                                                                                                                                                                                                                                                                     NLTPVTGRGKLLCILYALFGVPLILITVADIGKFLSENIV ( YTWYRKLREKCSKQKYSV 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEDLAVKYVDNVTRILFEAFDTHCIGAKHLRPGGEDEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSLIVLSVVYVGFGAFLFYQLEQPNEVEVRARNIERFNIHKPOMIEHLWEMRESGIGQHV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VYILTGLTVIGAFLNLV-----VLRFMTMNAEDEKRDA
                                                                                                                                                                                                                                                                                                                                                                                                           VKEANIKILPDDITEKDGYIVQNKS
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                                                                                                                                                                                                                                                         ITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVI. AFLNLVVLRFM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKKITSQYRSQSQSRSSSVMGSSKAGSMNLHDIDSDSE:
                                                                                                                                                                                                                 ITMTTVGFGDIVPLKR---
                                                                                                                                                                                                                                                                                                     ISSKDDKNKEGDLNLDHLENYISIPIFLIVAILLSYITFG . VLSMWEGWDFFSGFYFSF
                                                                                                                                                                                                                                                                                                                                             -AKKGLGMRRADVS---MANMVLIGFFSCI----STLCIG; \FSHYEHWTFFQAYYYCF 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QELRARY--NLSQGGYEELERVVLRLKPHKAG-----V
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78; Conserv
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ilarity 26.6%;
Conservative 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 293; DP:
Pred. No. 6e-1
57; Mismatches
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                                                                                                                                                                                                                 EYYILDLCYIIIGLSII MCIDLVGIQYI 299
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1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTALFFTTTLLTTIGYG 134
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                                                                  15-Oct-1999
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A;Reference number: Z19816
A;Accession: TZ3907
A;Status: preliminary; translat
A;Molecule type: DNA
A;Residues: 1-524 <WIL>
A;Cross-references: EMBL:Z74475
A;Experimental source: clone RC
C;Genetics:
A;Gene: CESP:R04F11.4
A;Map position: 5
A;Introns: 35/3; 83/2; 131/1; 1
                                                                                                                                                                                                                                                                                      hypothetical protein F20Al.7 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T30037 R;Gattung, S; Nu, X.
Q
                                                                                                                                                          A;Cross-references: EMBL:U53150; PIDN:AAA96127.1; GSPDB:GN00023; A;Experimental source: strain Bristol N2; clone F20A1
                                                                                                                                                                                                  A; Status: preliminary; translated A; Molecule type: DNA
                                                                                                                                                                                                                                A; Reference number: A; Accession: T30037
                                                                                                                                                                                                                                             submitted to the EMBL Data Library, March A;Description: The sequence of C. elegans A;Reference number: Z20726
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                            Best Loc
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Best Local Similarity
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;Introns: 35/3; 83/2; 131/1; 170/1; 261/1; 306/1; 338/1; 369/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:Z74475; PIDN:CAA98957.1; GSPDB:GN00023; CESP:R04F11.4 Experimental source: clone R04F11
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                                                        Query Match
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                            Local Similarity
mes 96; Conserv
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 8 TLALIVCTFTYLLVGAAVFDALESEPELIERQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTANDGMDELIRDVFWDYTRNYMTPDDVIYGDGPIKWSFMSSIFFSWTAITTIGYGHIVP 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AYIVRWEEWTFFEAFYFCFVTVTTIGFGDIVPANVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTDEGRVAIIFYALLGIPLILVTIADIGRFLATYIIKLHHGYMAVMSFVTNSCLKCIKWA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAAFSHYEHWTEFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RY-----LLHRAKK-----
                                                                                                  19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3;
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                         Score 268; DB 2
Pred. No. 6.2e-1
60; Mismatches 1
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Pred. No. 3.8e-17;
8; Mismatches 92
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cosmid F20A1
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                                                    Length 1539;
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R; Mortimore, B. submitted to the EMBL Data Library, *.pafarance number: Z19447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP:F31D4.7
A; Map position: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-443 <WIL>
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                                  IGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGA: _NIVVLRFMT---MNAEDEKR
                                                                               EMKEIERQERHDLDIFDLPLPVGIALIVTWIFICSFVLSVWDHNWTLLESFYFFFTSLST
                                                                                                                                                              PMTDAGRMLTMIFALFGIPLMLLVLQDFGKLLTITMKFFWFOIKRLMRRIMRCCTKQPIE 192
                                                                                                                                                                                                                                             KGNTSQRLTTFFIEELGSYEN----QLGVKWSQQKMDWDFWNAVLFAGTICTTIGYGHIY 132
                                                                                                                                                                                                                                                                                                                            LIIVFLIYCISGGLVFWLIEEPYQSELRDAWQHKIENNEFARVDAMMKKIFNNSDYLIYI 76
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                                                                                                                     -GMRRADVSMANMVL-IGFFSCISTLCIGAAAFSHYEH-WTFFQAYYYCFITLTT 199
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-PSSPRLLITMFGFILVGLSLVSN: !NLLOAKMKSTYEAGRNDEKT
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                                                                                                                                                                                                                                                                                      -GGYEELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAA 100
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Pred. No. '
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No. 4.7e :: 6;
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C; Genetics:
A; Introns:
                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-335 <AND>
                                                                                                                                                                        submitted to the EMBL Data A; Description: Sequence of A; Reference number: $44628
                                                                                                                                                                                                                                f22b7.7 protein - Caenorhabditis elegans c;Species: Caenorhabditis elegans C;Date: 20.reb-1995 #sequence_revision 20.ccession: S44635
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A;Status: preliminary; translated
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A;Title: ORK1, a potassium-selective leak channel with two po A;Reference number: 217770; MUID:97075152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             potassium channel protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
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                                                                                     A;Cross-references: EMBL:L12018; NID:g156298; C;Genetics:
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Best Local S
Matches 60
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Best Local Similarity
Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                              IALIPGIALFLLLPSWVFTYFENWPYSISLYYSYVTTTTIGFGDYVPTFGANQPKEFGGW 238
                                                                        18/3;
   60; Conserv
                                                                        79/1; 131/2;
    Conservative
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               12.7%;
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the C. elegans
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Pred. No. 1.4e-15;
5; Mismatches 107;
Score 259.5; DB 2;
Pred. No. 5.7e-16;
1; Mismatches 50;
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 A; Reference number:
               submitted to the EMBL
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hypothetical protein K01D12.4 - Caenorhabditis C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1 C;Accession: T23182
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A; Gene: CESP: ZK1067.5
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Pred. No. 9.4
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                   15-Oct-1999 #text_change 15-Oct-1999
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BL Data Z19703

Library,

June 1996

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-383 <WIL>
A;Cross-references: EMBL:275543; PIDN:CAA99871.1; G:
A;Experimental source: clone K01D12
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A;Map position: X
A;Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3
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A; Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2
                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z78541; PIDN:CAB01740.1; GSPDB:GN00028; CESP:F19D8.1 A;Experimental source: clone F19D8
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A; Residues: 1-452 <WIL>
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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93 IAKLATTENVAE--INEHLRMFLRNISNLHISLDNYLIFNEPTQIVPKR----WTFPSSV 146
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                                       MKFRNVLRIALGHLALYCFVVC---YVFAGAWVFHQLEGENETELHDKQREYAMNLKKDV 92
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Search completed: August 28, 2001, 17:07:06 Job time: 475 sec

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  This SWISS-PROT entry is copyright. It is good and through a collab between the Swiss Institute of Bioinformat. And the EMBL outst the European Bioinformatics Institute. The content is in use by non-profit institutions as long as its content is in modified and this statement is not removed. Assage by and for comparations are the statement in the content is in the content in the content in the content is in the content in the content in the content is in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content in the content i
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RESULT 1 CIW3_HUMAN TANDARD; PRT; 394 A/. ID CIW3_HUMAN STANDARD; PRT; 394 A/. AC 014649; DT 01-OCT-2000 (Rel. 40, Last sequence update; DT 01-OCT-2000 (Rel. 40, Last sequence update; O1-OCT-2000 (Rel. 40, Last annotation update; O1-OCT-2000 CRAL 40, Last annotation update; O1-OCT-2000 (Rel. 40, Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; VeEukaryota; Eutheria; Primates; Catarrhini; i MEDLINE=97459932; PubMed=9312005; Duprat F., Lesage F., Fink M., Reyes "TASK, a human background K+ channel near physiological pH."; EMBO J. 16:5464-5471(1997). MEDLINE-99254548; PubMed-10321245; Patel A.J., Honore E., Lesage F., Fink M., "Inhalational anesthetics activate two-porc NCBI_TaxID=9606; SEQUENCE FROM N.A. Neutosci. 2:422-426(1999). FUNCTION: PH-DEPENDENT, VOLTAGE-INSENS. V. BACKGROUND POTASSIUM FUNCTION: PH-DEPENDENT, VOLTAGE-INSENS. V. BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTI.: PASSUES FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE PASSUES FROM POTASSIUM CONCENTRATION V. PASSUES FROM IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION V. PASSUES CUPRENTIAL). SUBCELLULAR LOCATION: INTEGRAL MEMBRANI V. P. P. (POTENTIAL). SUBCELLULAR LOCATION: INTEGRAL MEMBRANI V. P. P. (POTENTIAL). TISSUE SPECIFICITY: WIDESPREAD EXPRESS V. PADULT. STRONGEST EXPRESSION IN PANCREAS AND PLACENTA. L. V. PRESSINE AND COLON. LUNG, PROSTATE, HEART, KIDNEY, UTENUS. V. L. INTESTINE AND COLON. LUNG, PROSTATE, HEART, RUDBEY PRESSION IN ACCITATION ACTIVATED BY LUNG, PROSTATE, HEART, KIDNEY, DIENDO, MISCELLANEOUS: INHIBITED BY EXTERNAL AND ISOFLURANE. HALOTHANE AND ISOFLURANE. SIMILARITY: BELONGS TO THE TWO PORE DO ALIGNMENTS ς, ser external pH variations ₹. 4/3 G., Lazdunski ・合う TRIVE POTASSIUM い () 以 K+ CHANNEL). n-lae; · AMILY OF POTASSIUM and the EMBL outstation -Euteleostomi; Lazdunski M.; ackground K+

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MEDLINE-98099797; PubMed-9437008;
Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H.,
Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;
"An open rectifier potassium channel with two pore dome
                                                                                                                    01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE POTASSIUM CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CHANNEL).
                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
MCBI_TaxID=10116;
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Pfam; PF02034; TWIK_channel; 1
PRINTS; PR01095; TASKCHANNEL.
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InterPro; IPR001622; ...
InterPro; IPR003092; ...
InterPro; IPR003280; ...
Pfan; PF02034; TWIK_Channel; 1.
PRINTS; PR01095; TASKCHANNEL.
PRINTS; PR01333; 2POREKCHANNEL.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              cloned from rat cerebellum.";
J. Neurosci. 18:868-877(1998)
-i- FUNCTION: PH-DEPENDENT, V
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                                             YERWITEFQAYYYCFITLTTIGFGDYVALQKDQALQTQFQ, CFYYYLLTGLTVIGAFLN
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MW; D2778016E09E2+** CRC64;
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3; Mismatches
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE F CONNECTION OF TABLE 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20287574; PubMed-10748056; Lopes C.M., Gallagher P.G., Buck M.E. "Proton block and voltage gating are cardiac leak channel kcnk3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim D., Fujita A., Horio Y., Kurachi Y
"Cloning and functional expression of
background K+ channel (cTBAK-1).";
Circ. Res. 82:513-518(1998).
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                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Puprat F., Lesage F., Fink M., Reyes "TASK, a human background K+ channel near physiological pH."; EMBO J. 16:5464-5471(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 4-409 FROM N.A. MEDLINE-97459932; Pubmed-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=20287574;
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Kim D., Fujita A., Horio Y., Kura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Heart;
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CARDIAC TWO-PORE BACKGROUND KCNK3 OR TASK OR CTBAK.
                                                                                                                                                                                                                                                                                                          between
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- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIT CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON ETHER SIDE OF THE MEMBRANE. ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.

WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARI
                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.

MISCELLANEOUS: INACTIVATED BY BARIUM.

SIMILARTIY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM CHANNELS.
                                                                                                                                                                                                                                           ween the Swiss Institute of Bioinforma
European Bioinformatics Institute. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         musculus (Mouse)
AB008537; BAA25436.1;
AF006824; AAC53367.1;
AB013345; BAA28349.1;
AE241799; AAF81418.1;
AF242508; AAF81418.1;
                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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                                                                                                                                                                 requires a license agreement (See http://www.an email to license@isb-sib.ch).
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        JOINED
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; Murinae; Mus
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pH variations
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RESULT (
CIW2_MOUSE STANDARL,

ID CIW2_MOUSE STANDARL,

AC P97438;

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update) i

DT 01-OCT-2000 (Rel. 40, Last annotation update v.

DT 01-OCT-2001 (Rel. 40, Last annotation update v.

DE POTASSIUM CHANNEL SUBGRAMILY K MEMBER 2 (OUTWARD) v. (CTANNEL PROTEIN TREK-1) (TWO-PORE POTASSIUM ANNEL CHANNEL SUBUNIT).

CHANNEL SUBUNIT).

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InterPro;
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IPR001622;
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PORE-FORMING
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PORE-FORMING
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V -> I (IN REF. 35236E011AAC5
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               Euteleostomi;
Murinae; Mus
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Matches 109; Conserv
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SEOUENCE FROM N.A., F
TISSUE-Brain;
MEDLINE-97157476; Pu
Duprat F.,
                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                  Ionic channel; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fink M., Duprat
Lazdunski M.;
                                                                                                        SEQUENCE
                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                      TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           channels."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patel A.J., Honore E., Les
"Inhalational anesthetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99254548; PubMed=10321245; Patel A.J., Honore E., Lesage F., Fink M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBO J. 15:6854-6862(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lazdunski M.;
"Cloning, functional
                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HONODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENT SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN LUNG. TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULLIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULLIVER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIPPOCAMPUS AND CEREBELLUM.
MISCELLANEOUS: INHIBITED BY BARIUM.
ANAESTHETICS SUCH AS CHLOROFORM, DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: OUTWARD RECTIFYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:109366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (APR-1999)
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    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane;
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28.0%;
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                                                                                                                          N-LINKED
                       Score 370; DB 1;
Pred. No. 2.1e-22;
                                                                                                                                                                                      SENSITIVITY
                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
ESSENTIAL FOR CHLOROFORM AND
                                                                                                                                                                  REQUIRED FOR BASAL CHANNEL ACTIVITY
                                                                                                                                                                                                                                                                       POTENTIAL.
PORE-FORMING
                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL)
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-LINKED (GLCNAC. . .)
8F976DDD103EFA05 CRC
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    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fink M., Romey G., Lazdunsk:
  two-pore-domain background
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brain localization
channel.";
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                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                       Potassium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
                                      Length 411
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modified and this statement is not removed.
entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                           Price L.A., Hellings S.E., Hayashi J.H., Pa::ch M.H.: Submitted (MAY-1997) to the EMBL/GenBank/DD: databases.
-!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
-!- SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                 This
                                                                                                                                                                                                                :- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
-!- MISCELLANEOUS: ACTIVATED BY VOLATILE GERENAL ANAESTHETICS S
-:- CHLOROFORM, HALOTHANE AND ISOFLURANE.
-!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN I AMILY OF POTASS.
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                                                                                                                  s SWISS-PROT entry is copyright. It is produced the Swiss Institute of Bioinformatics European Bioinformatics Institute. There are
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-RELATED STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
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MIM; 6
                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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        SEQUENCE FROM
                        NCBI_TaxID=9606;
                                                           Homo sapiens (Human).
                                                                     KCNK4 OR TRAAK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2POREKCHANEL.
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283
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                                       Primates;
                                                Chordata;
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30.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                               61;
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N-LINKED (GLCNAC. . .) (PO)
MISSING (IN REF. 2)
MISSING (IN REF. 2).
S -> N (IN REF. 2).
A -> T (IN REF. 2).
A -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 6.7e-22;
1; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 364; DB 1;
Pred. No. 6.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESSENTIAL FOR CHLOROFORM AND HALOTHANE SENSITIVITY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
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                                       Catarrhini;
                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ion transport; Potassium
                                                                                                                                             393
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A
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                                       Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                       Homo
                                                                                          ARACHIDONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transport;
                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                  335
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                                                                                          ACID-
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Best Local
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Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M., Kelsell R.E., Murdock P.R., Randall A.D., Penn e G.I., Gloger I.S., "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potasses, in channel.";
Brain Res. Mol. Brain Res. 82:74-83(2000).
                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is proved through between the Swiss Institute of Bioinformat by and the Electropean Bioinformatics Institute. The the European Bioinformatics Institutes by non-profit institutions as long and the secontent modified and this statement is not removed. They are by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF248242; AAG31731.1; EMBL; AF247042; AAF64062.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray A.T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ionic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                         224
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE 'SIMILARITY: BELONGS TO THE TWO PORE DOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: VOLTAGE INSENSITIVE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: VOLTAGE INSENSITIVE, INSTANTANT : POTASSIUM CHANNEL OUTWARD RECTIFICATION : R
                                                                                                                                                                                                                                                                     ALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRKA
                                                                                                                                                                                                                                               LALLALVLLYLVSGALVFRALEQPHEQQAQRELGEVREKF, AHPCVSDQELGLLIKEVA 66
                       SFVYILTG----
                                                                                                                                                                                   DALGGGADPETNSTSNSSHSA---WDLGSAFFFSGTIT () YGNVALRTDAGRLFCIFY
                                                    LIGCLLFVLTPTFVFCYMEDWSKLEAIYFVIVTLTTVGF;51YVAGADPR--QDSPAYQPL
                                                                                  FFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGF ; DYVALQKDQALQTQPQYVAF
                                                                                                                 ALVGIPLFGILLAGVGDRLGSSLRH-----GIGHIEA : KWHVPPELVRVLSAMLFL
                                                                                                                                                                                                                 ---GGYEELERVVLRLKPHKAGVQWRFAGSFYFAITVITT , YGHAAPSTDGGKVFCMFY
                                                                                                                                                                                                                                                                                                                 98;
                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR01333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cortex;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF64062.1;
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LTVIGAFLNLVVLRFMTMNAEDUS (ABHRALLTRNGQAGGGGGG
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                                                                                                                                                                                                                                                                                                                               Score 329.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
P -> L (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC
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PORE-FORMING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                 7F18E53A0A9AD57D CRC64;
                                                                                                                                                                                                                                                                                                                 Mismatches
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PORE DOMA 9 "AMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                 3.4e;19;
hes 112;
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                                                                                                                                                                                                                                                                                                                                                 393;
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RESULT 7
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                               Glycoprotein;
DOMAIN
                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                 the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTASSIUM CHANNEL SUBFAMILY K MEMBER 4 (TWIK-F STIMULATED POTASSIUM CHANNEL PROTEIN) (TRAAK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (Rel. 01-OCT-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CIW4_MOUSE O88454;
                TRANSMEM
                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                between
                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A neuronal two P domain K+ channel polyunsaturated fatty acids."; EMBO J. 17:3297-3308(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCNK4 OR TRAAK.
Mus musculus (Mouse)
                                                                                   Pfam; PF02034; TWIK_channel; 1.
                                                                                                                                                           EMBL; AF056492; AAC40181.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99254548; PubMed=10321245; Patel A.J., Honore E., Lesage F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                        Ionic
                                                                      PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                  [nterPro;
                                                                                                                 [nterPro;
                                                                                                                              InterPro; IPR000099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patel A.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    azdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fink M., Lesage F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98292450;
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND
2/TRAAKT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPELICING.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE.
DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
                                                                                                                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                          CHANNELS
                                                                                                                                                                                                                                                                                                                    FATTY ACIDS: NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE. SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASS
                                                                                                                                                                                                                                                                                                                                                               MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER (POTENTIAL).
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                                                                                                                                               MGI:1298234;
                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                       S; PR01333; 2POREKCHANEL. channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurosci.
                                                                                                                                                                                                                                                             the Swiss Institute of Bioinformatics
                                                                                                  IPR003280;
                                                                                                                 IPR001622;
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; Alternative : 1 3 4 24 89 113
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                                                                                                                                            Kcnk4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=9628867;
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40. Last annotation update)
SUBFAMILY K MEMBER 4 (TWIK-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duprat
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                                         splicing
                            CYTOPLASMIC (POTENTIAL).
PORE-FORMING (POTENTIAL)
                                                        Ion transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fink M., Romey G., Lazdunsk
e two-pore-domain background
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398
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                                                        Potassium
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                                                                                                                                                                                                                                                                                                                      OF POTASSIUM
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RESULT 8
CIW1_HUMAN
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Best Local Similarity
                                                                                                                                                                                                                                                                             000180; Q13307;
01-OCT-2000 (Rel. 4
01-OCT-2000 (Rel. 4
01-OCT-2000 (Rel. 4
                                J. Mol.
[3]
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                         01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update,
POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWA)
CHANNEL PROTEIN TWIK-1) (POTASSIUM CHANNEL K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
VARSPLIC
   Desir G.V., Orias M., Submitted (APR-1997)
              SEQUENCE FROM Desir G.V., Or
                                                                   MEDLINE=98122696;
Goldstein S.A.N.,
                                                                                         TISSUE-Brain;
                                                                                                 SEQUENCE FROM
                                                                                                                      EMBO
                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Verte:
Mammalia; Eutheria; Primates; Catarrhini; Hom.
NCBT Tastrococo.
                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                   KCNK1 OR TWIK1 OR HOHO1 OR KCNO1.
                                                                                                                                                                                                                                                                                                                     CIW1_HUMAN
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                                                                                                                               novel structure
                                                                                                                                                            Lesage F.,
                                                                                                                                                                     MEDLINE=96183184;
                                                                                                                                                                                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                  implications
                                                                                                                                       "TWIK-1, a ubiquitous human
                                                          Soldstein S.A.N., Wang K.-W., Ilan North Sequence and function of the two P
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                                   of an emerging superfamily."; 76:13-20(1998).
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31.5%;
Freeman T.;
to the EMBL/GenBank/DDBJ databases
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Pred. No. 6.1e-1
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N-LINKED (GLCNA (M. .)) (POTENT
KLLVE -> KAMAI (M. ISOFORM 2).
MISSING (IN ISOFORM 2)
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                                                            channels:
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RESULT 9
CIW5_HUMAN
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Best Local
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MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001622;
InterPro; IPR001779;
InterPro; IPR003280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000099;
                                                                                                                                                                 146
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                                                                                                                                                                                                                                                                                          11 LIVCTFTYLLVGAAVFDALESEPELIERQRL-ELRQQELRARYNLSQGGYEELERVVLRL
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HE
BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND
INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHANNELS
                                                                                        TG----LTVIGAFLNLVVL---
                                                               LGLIAMLVVLETFCELHELKKFRKMFYVKKDKDEDQVH
                                                                                                                                      AAAFSHYE-HWTFFQAYYYCFITLTTIGFGDYVA----LQKDQALQTQPQYVAFSFVYIL
                                                                                                                                                               LLFLTAVVQRIT-----VHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIP
                                                                                                                                                                                       LVMFQSLGERINTLVRYLLHRAKKGL------GMRRADVSMANMVLIGFFSCISTLCIG
                                                                                                                                                                                                                   SNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFT
                                                                                                                                                                                                                                                                  LVLGYLLYLVEGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEA
                                                                                                                AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFREL---
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                                                                                                                                                                                                                                                                                                                     Conservative
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212
247
268
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  STANDARD;
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                                                                                                                                                                                                                                         -QWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLT
                                                                                                                                                                                                                                                                                                                                15.7%;
                                                                                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                     47;
                                                                                                                                                                                                                                                                                                                                Score 320.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POI
T->A: NO EFFECT ON CHANNEL
; 2A41D9501323215D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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  PRT;
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nes 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transport;
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Matches 84
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01-OCT-2000 (
                                                                                                                                      TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                       TRANSMEM
DOMAIN
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J. Biol. Chem. 273:30863-30869(1998).
-i- FUNCTION: PH DEPENDENT, VOLTAGE INSENS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 5 (ACL. SECHANNEL PROTEIN TASK-2) (TWIK-RELATED ACLD-: FNSCHANNEL PROTEIN TASK-2)
                                                                                                                                                                                                                                                                           Pfam; PF02034; TWIK_channel; 1 PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is pubetween the Swiss Institute of Bioinformatic the European Bioinformatics Institute. The
                                                                                                                                                                                                                                                                                                                                    MIM; 603493;
                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                     Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99030343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCNK5 OR TASK2
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                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                [onic channel;
                       15
  67
                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANT DE "EIN (POTENTIAL).
TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT EXPRESSED IN PROXIMAL TUBULES OR GLOMERUL!)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: INHIBITED BY QUININE, QUINTUDINE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACIDIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K+ CONCENTRATIONS.
--LRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAP: [*** KVFCMFYALLGIPLTLVM
                        YLAIGAAIFEVLE-EPHWKEAKKNYYTQKLHL----LK'
                                             YLLVGAAVFDALESEPELIE ---- RQRLELRQQELRA ...
                                                                  Similarity 32.8
84; Conservative
                                                                                                                                                                                                                                                                                                 IPR003280;
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                                                                   15.6%; Score 319; Did 32.8%; Pred. No. 3.1: ...
ive 47; Mismatches
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Catarrhini; Home idae;
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O1-0CT-2000 (Rel. 40, Last annotation update)
O1-0CT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INF
between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for come entities requires a license agreement (See http://www.ish-cib.ch.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCNKI.
Mus musculus (Mouse).
Mus musculus (Mouse).
""karyota; Metazoa; Chordata;
""karyota; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure, chromosome localization, omnuse twik K+ channel gene.";
FEBS Lett. 425:310-316(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129/SVJ; TISSUE=Liver; MEDLINE=98218573; PubMed=9559671;
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Lazdunski M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
TISSUE SPECIFICITY: WIDELY EXPRESSED HIGHEST EXPRESSION IN
KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE
EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TES
                                                                                                                                                                                                                        MISCELLANEOUS: INHIBITED BY QUI
ACIDIFICATION. ACTIVATED BY PRO
SIMILARITY: BELONGS TO THE TWO
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CONCEPTION. EXPRESSION STABILIZES AFTER DAY
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RESULT 11

CIW6_HUMAN STANDARD; PRT; 313 AA.

ID CIW6_HUMAN STANDARD; PRT; 313 AA.

AC 09Y257;

DT 01-OCT-2000 (Rel. 40, Created)

DT 01-OCT-2000 (Rel. 40, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last senotation update)

DT 01-OCT-2000 (Rel. 40, Last senotation update)

DT 01-OCT-2000 (Rel. 40, Last senotation update)

DE POTASSIUM CHANNEL SUBFAMILY K MEMBER 6 (INWARD RECTIFYING DE CHANNEL PROTEIN TWIK-2) (TWIK-ORIGINATED SIMILARITY SEQUEN KCKK OR TWIK2 OR TOSS.
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CARBOHYD
          Pountney D.J., Gulkarov I., Vega-Saenz de Miera E., Holmes D., Saganich M., Rudy B., Artman M., Coetzee W.A.:
"Identification and cloning of TWIK-originated similarity sequence (TOSS): a novel human 2-pore K+ channel principal subunit.";
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                                          MEDLINE=99285568; PubMed=10359073;
Pountney D.J., Gulkarov I., Vega-Saenz de Mieta E.,
                                                                              SEQUENCE FROM N.A.
                                                                                             NCBI_TaxID=9606;
[1]
                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF02034; TWIK_channel;
                                                                                                                   Mammalia;
                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ionic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                         200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 LIVCTFTYLLVGAAVFDALESEPELIERQRL-ELRQQELRARKNLSQGGYEELERVVLRL 69
Lett.
                                                                                                                                                                                                                                                                                            LGLITMLVVLETFCELHELKKFRKMFYVKKDKDEDLVH
                                                                                                                                                                                                                                                                                                                  TG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:109322; Kcnkl.
                                                                                                                                                                                                                                                                                                                                         AAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYN
                                                                                                                                                                                                                                                                                                                                                             AAAFSHYE-HWTFFQAYYYCFITLTTIGFGDYVA----LCI AQALQTQPQYVAFSFVYIL
                                                                                                                                                                                                                                                                                                                                                                                                            LVMFQSLGERINTLVRYLLHRAKKGL-----
                                                                                                                                                                                                                                                                                                                                                                                      LLFLTALVQRVT-----VHVTRRPVLYFHIRWGFSKQVV8.VHAVLLGFVTVSCFFFIP
                                                                                                                                                                                                                                                                                                                                                                                                                                   SNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGYGHTVPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPHKAGV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVLGYLLYLVFGAVVFSSEELPYEDLLRQELRKLKRRFLEPHECLSEPQLEQFLGRVLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF033017; AAC16973.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003280; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001622; -. IPR001779; -.
 novel human 2-pore K+ channel 450:191-196(1999).
                                                                                                                             Metazoa;
                                                                                                                                                                                                                                                                                                                  LTVIGAFLNLVVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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21
104
133
154
178
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268
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41
130
153
177
198
238
267
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                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38275
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                                                                                                                                                                                                                                                                                                                  REMIMNAEDEKRDAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (P'POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 318.
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PORE-FORMING (
                                                                                                                   Catarrhini;
                                                                                                                             Craniata; Vertebrata; Euteleostomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A996060A18266FD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318.5; DB 1
No. 2.2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                             -GMRRADV.
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                                                                                                                   Hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1 .: ENTIAL)
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                                                                                                                                                                                                                                                                           . 5%
                                                                                 ni idae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              otassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YTTAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 'GGKAFCIIYSVIGIPFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XTIAL).
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                                                                                                                                                                 SEQUENCE)
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                                                                                                                                                                                                                                                                                                                                         YKIGITCYLL
                                                                                                                                                                           POTASSIUM
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                                                                                                                                                                  Matches
                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mehta Y., Forsayeth J. R., Yost C.S., J. Biol. Chem. 274.24440-22440(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR001779; -
InterPro: IPR001779; -
PRINTS; PR01096; TWIK1CHANNEL.
Tonic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chavez R.A., Gray A.T., Zhao B.B., Kir
Mehta Y., Forsayeth J.R., Yost C.S.;
"TWIK 2, a new weak inward rectifying
potassium channel family.";
                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF1177
MIM; 603939;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF134149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERRATUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99175162; PubMed-10075682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                   MUTAGEN
                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001622;
                             121
                                                                                                                                                                            Local
                                                        74
                                                                                 64
                                                                                                            17
                                                                                                                                     18 YLLVGAAVFDALESEPELIERQRLELRQQELRARYN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS. LOWEST EXPRESSION DETECTED IN BRAIN.
MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARIUM.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAD EXPRESSION, DETECTISSUE SPECIFICITY: WILDESPREAD EXPRESSION, DETECTISTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXP
 TMLLLTASAQRLSLL---LTHVPLSWLSMRWGWDPRRA---
                           TLVMFQSLGERINTLVRYLLHRAKKGLGM-----RRADVSMANMVLIGFFSCISTLC--
                                                       RVVLANASGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPT
                                                                                                            YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCVAAPALDAFVERVLAAG----RLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF117708;
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chem. 274:7887-7892(1999)
                                                                                                                                                                                                                                   90
121
142
173
199
236
257
79
85
85
313
                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD22980.1;
AAD24000.1;
                                                                                                                                                                                                                                  4
25
115
114
172
193
223
223
226
313
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85
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND MUTAGENESIS OF CYS-53.
                                                                                                                                                                             14.5%;
31.7%;
                                                                               WRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL
                                                                                                                                                                                                                                    ₹.
                                                                                                                                                                  40;
                                                                                                                                                                             Score 295.5;
Pred. No. 1.
                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).

"LINKED (GLCNAC. ..) (PO
N-LINKED (GLCNAC. ..) (PO
C->A: NO CHANNEL ACTIVITY.
; 1379382DFB0575DE CRC64;
                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PORE-FORMING (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                             Ion transport;
                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kindler C.H., Mazurek M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               member of the tandem pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRONGEST EXPRESSION IN
                                                                                                                                                               1.4e-16;
hes 95;
                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as its content
                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                             Potassium
                                                                                                                                  LSQGGYEELE
-ACWHLVALLGVVVTVCFL
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                                                                                                                                                                Indels
                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                (POTENTIAL)
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                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                             transport;
                                                                                                                                                                                           313;
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                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUES
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in no way
commercial
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 186
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RESULT 12
ORK1_DROME
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      RA George R.A. Lewis S.E., Richards S. Ashburn. M. Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhan- Q., Chen L.X., RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., C., The M., Pfeiffer B.D., RA Wan K.H., Doyle C., Baxter E.G., Helt G., No. 2nd C.R., Mixlos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews- trakoch C., Baldwin D., RA Ballew R.M., Basca A., Baxendale J., Bayrakt. C., Inches R. R. Besson K.Y., Benos P.V., Berman B.P., Bhand. D., Brottier P., RA Berson K.Y., Benos P.V., Berman B.P., Bhand. C., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokste C., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokste C., Brottier P., RA Borkova D., Botchan M.R., Bouck J., Brokste C., Brottier P., Brottier P., Benos P.V., Berman B.P., Bhand. C., Brottier P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brokste C., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brottier P., Brotti
Ye J., i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
OPEN RECTIFIER POTASSIUM CHANNEL PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goldstein S.A.N., Price L.A., Rosenthal D.N., Fousch M.H.; "ORK1, a potassium-selective leak channel with "wo pore doctioned from Drosophila melanogaster by expression in Sacch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Proda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORK1_DROME Q94526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M.D., Celniker S.E., Holt R.A., Ev
Amanatides P.G., Scherer S.E., Li P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 93:13256-13261(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97075152; PubMed=8917578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187
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- FUNCTION: BACKGROUND POTASSIUM CHANNEL.
ON EXTERNAL POTASSIUM CONCENTRATION. ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL)
TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT, STRONGE
EXPRESSION IN MUSCLE, BRAIN AND OVARY. ALSO PRESENT AT LOW
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SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
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Drosophila melanogaster.";
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Pred. No. 2.7
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CIN7_HUMAN STANDARD; PRT; 3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is provided the collable tween the Swiss Institute of Bioinformatic There is the European Bioinformatics Institute. There is the European Bioinformatics Institute. There is content is in modified and this statement is not removed. The entities requires a license agreement or send an email.
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MEDLINE=94150718; PubMed=7906398;
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Rhabditidae; Peloderinae;
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TWK-8 OR F22B7.7
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SEQUENCE
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J. Biol. Chem. 274:11751-11760(1999).

-i- FUNCTION: PROBABLE POTASSIUM CHANNEL SUBUNIT. NO CHANNEL ACTIVITY OBSERVED IN VITRO AS PROTEIN REMAINS IN THE ENDOPLASMIC RETICULUM.
MAY NEED TO ASSOCIATE WITH AN AS YET UNKNOWN PARTNER IN ORDER TO
                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Ionic channel;
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             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PRO
ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRODUCED BY ALTERNATIVE SPLICING SIMILARITY: BELONGS TO THE TWO
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                                   TQAHGVSTLGNSSEGRTWDLPSALLFAASILTTTGYGHMAPLSPGGKAFCMVYAALGLPA 132
                                                                                LVVAHLLALGLGAVVFQALEGPPACRLQAELRAELAAFQAEHRACLPPGALEELLGTALA 72
                                                                                                                                Similarity
77; Conserv
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                                        KAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL 120
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R., Lesage F., F
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31946 MW;
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(IN ISOFORM C)
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N-LINKED (GLCNAC. . ) (
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..
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BD4A36DD9591ADAC CRC64;
                                                                                                                                Mismatches 116;
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No. 6.8e-11
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SUBMITTED

IN VITO AS PROTEIN REMAINS IN "HE ENDOPLASMIC RETICULUM
MAY NEED TO ASSOCIATE WITH AN AS YET UNA"; AN PARTNER IN ORDER TO
REACH THE PLASMA MEMBRANE.

I SUBUNIT: HOMODIMER (POTENTIAL).

TISSUE SPECIFICITY: DETECTED IN EMBRYO.

WEAKLY EXPRESSED IN COLON, TESTIS, ATRIA, IDNEY, INTESTINE,
BLADDER, UTERUS, OVARY, SALIVARY GLAND.

HEART, VENTRICLE,
UTERUS, OVARY, SPINAL CC. HEART, VENTRICLE,
BLADDER, UTERUS, OVARY, SPINAL CC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9Z2T1; Q9R242; QYKIVI, CTC
01-CCT-2000 (Rel. 40, Created)
01-CCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 8 (PUTATED TO THE POTATED TO THE SUBFAMILY K MEMBER 8 (PUTATED TO THE POTATED                                                                                                                                                                                                                                                                                                                                                                                                                 Gan L., Joiner W.J., Kaczmarek L.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 2-307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bockenhauer D., Gallagher P.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning of a new mouse two-P domain chann-
homologue with a unique pore structure.";
J. Biol. Chem. 274:11751-11760(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salinas
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CIW8_MOUSE
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                                                                                                                                                                                                                                                                                                                   TISSUE-Brain;
Lopes C.M.B.,
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 15-307 FROM N.A.
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                                 DETECTED IN BRAIN, CEREBELLUM, SPINAL CC. HEART SKELETAL MUSCLE, LIVER, PLACENTA AND PAN "EAS. IN EXPRESSED IN THE RETINAL GANGLION CELL IT," R AND
SIMILARITY:
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                                                                                                                                                                                                                                                                                                                     Buck M.,
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Sciurognathi; Invidae;
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Best Local Similarity
Matches 76; Conserv
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EMBL; AB015729; BAA35074.1; --
EMBL; AF022820; AAD09337.1; --
EMBL; AF012324; AAF21603.1; --
EMBL; AF012324; AAF21603.1; --
EMBL; AF158234; AAF14528.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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InterPro; IPR003280;
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                                                                                                                       115 LIGIPLITLVMFQSL------GERINTLVRYLLHRAKKGLGMRRADVSMANMVLIG 163
237 ALLGYLLLGLLAMLLAVETFSELPQVRAMVKFFGPSGSRTDEDQD
                          221 VAFSFVY--ILTGLTVIGAFLNLVVLRFMTM-----NAEDEKRD 257
                                                                            164 FFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQ---KDQALQTQPQY 220
                                                                                                          127
                                                                                                                                                            69 AVLRAQAH -- GVSSLGNGSETSNWDLPSALLFTASILTTTGYGHMAPLSSGGKAFCVVYA 126
                                                                                                                                                                         7 RTLALIVCTFTYLLVGAAVFDALESEP--ELIERQRLELRQQELRARYNLSQGGYEELER 64
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                                                                                                        ALGLPASLALVAALRHCLLPVFSRPGDWV--AIRWQLAPAQAAL-----LQAAGLGLL-
                                                     -VACVFMLLPALVLWGVQGDCSLLEAIYFCFGSLSTIGLGDLLPAHGRGLHPAIYHLGQF
                                                                                                                                                                                                                RYLLLLMAHLLAMGLGAVVLQALEGPPARHLQAQVQAELASFQAEHRACLPPEALEELLG 68
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26.7%;
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N-LINKED (CLORG. . . . ) (FULL. . . . . . . . . . . )

MGS -> TR (IN REF. 4).

GS -> TR (IN REF. 4).

GS -> THSREFGPROGEFGTR (IN REF. 2).

G -> SP (IN REF. 2, 3, 4 AND 5).

"" -> SP (IN REF. 2).
                                                                                                                                                                                                                                                                  ; Score 221; DB 1;
; Pred. No. 1.2e-10;
44; Mismatches 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
PORE-FORMING (POTENTIAL).
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POTENTIAL.
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-> P (IN REF. 2).
567D32AE355BA44F CRČ64;
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Search completed: August 28, Job time: 409 sec

2001, 17:13:15

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Title:
Perfect score:
Sequence:
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: sp_archea:*
2: sp_bacteria
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5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe!
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Match
      84.8
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Copyright (c) 1993 - 2000 Com
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Q9j158 cavia porce
Q9j164 rattus norv
Q9es08 rattus norv
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Q9hbc8 homo sapien
Q9h427 homo sapien
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Q9h428 denorhabdi
Q17185 caenorhabdi
Q17185 caenorhabdi
Q9j157 cavia porce
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Q9j157 cavia porce
Q9nrt2 homo sapien
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE POTASSIUM CHANNEL DP4 (FRAGMENT).
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InterPro; IPR003280; -.
Pfam; PF02034; TMIK channel; 1
PRINTS; PR01333; 2POREKCHANEL.
PRINTS; PR01095; TASKCHANNEL.
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Submitted (SEP-1997) to the
EMBL; AF022821; AAD09338.1;
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01-MAY-2000
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InterPro; IPR001622; -.
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Sciurognathi;
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01-MAR-2001 (
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TWIK-RELATED
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Homo sapiens (Human).
""karyota; Metazoa; Chordata;
""heria; Primates;
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Girard C., Lesage F.,
"Human Task-3, a novel
Submitted (JUN-2000) 1
                                                                                                                                                                                                                                                                                                                                                                   Q9NPC2 PRELIMINARY; PRT; 374 AA. (2)
Q9NPC2;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TREMBLREL TASK-3 (POTASSIUM CHANNEL TASK3)
Q1-MAR-2001 (TREMBLREL TASK-3)
Q2-MAIN POTASSIUM CHANNEL TASK3)
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Ionic channel.
SEQUENCE 301 AA; 32811 MW;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                 SEQUENCE FROM N.A. MEDLINE=20287530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohya S., Kitsukawa M., Imaizumi Y.;
"TWIK-related acid-sensitive K+ channel
                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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(TremBirel. 16, Last sequence update)
(TremBirel. 16, Last annotation phase)
D ACID-SENSITIVE K+ CHANNEL SPRICE VARIANT
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                                                                                    PubMed=10747866;
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EMBL/GenBank/DDE.
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Pred. No. 8.8e
6; Mismatches
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Best Local Similarity
Matches 233; Conserv
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Karschin A., Derst C.;
"TASK-3, a novel tandem proe domain aciextracellular histidine as pH sensor." " "inl. Chem. 275:16650-16657(2000)."
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BMBL; AF21829; AAF63708:1; -.

EMBL; AF257080; AAG33126:1; -.

EMBL; AF248241; AAG31730.1; -.
 Q9JL58
Q9JL58;
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InterPro; IPR003280; -.
Pfam; PF02034; TMIK_channel; 1.
PRINTS; PR01333; 2POREKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
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and KT3.3
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          PRELIMINARY;
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           PRT;
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Best Local Similarity 57.1
Matches 226; Conservative
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InterPro; IPR003280; -.
Pfam; PF02034; TWIK_channel; 1.
PRINTS; PR01333; 2POREKCHANNEL.
PRINTS; PR01095; TASKCHANNEL.
SEQUENCE 365 AA; 40769 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000
01-OCT-2000
01-MAR-2001
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extracellular histidine as pH sensor."
J. Biol. Chem. 275:16650-16657(2000).
EMBL; AF212827; AAF63706.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20287530; PubMed=10747866; Rajan S., Wischmeyer E., Liu G.X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000099;
InterPro; IPR001622;
InterPro; IPR003092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10141;
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Last sequence Last anno
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Pred. No. 1.9
43; Mismatches
                                                                                                Created)
Last sequence up
Last annotation
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Hystricognat
         Craniata; Ver
Sciurognathi
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Best Local Sim
Matches 174;
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                                                                                                           Ionic channel.
NON_TER 23
SEQUENCE 237
                                                                                                                                                                                                                                                                                                                                                                                                                                       O9ESO8;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
TWO PORE POTASSIUM CHANNEL KT3.2 (FRAGMENT).
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EMBL; AF192366; AAF60229.1; InterPro; IPR000099; INFORMATION INFORMATION.
                                                                                                                                                                                                                                     "KT3
                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE-DAWLEY;
Vega-Saenz de Miera E.C.,
                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF02034; TWIK_channel; 1
PRINTS; PR01333; 2PONEKCHANEL.
PRINTS; PR01095; TASKCHANNEL.
SEQUENCE 395 AA; 44365 MW;
                                                                                                                                                                   Submitted (APR-2000) to the EMBL; AF257082; AAG33128.1;
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.2 and KT3.3 Two Novel Human Two
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                          Similarity
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237 t
      Conservative
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26674 MW;
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73.4%;
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                                                                                                                                                                                           EMBL/GenBank/DDBJ
                        Score 924; DB 1
Pred. No. 8e-74;
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    Mismatches
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Best Local
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Q9H427;
Q9H427;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                     Q9HBC8
Q9HBC8;
Q1-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                           Submitted (APR-2000) to the EMBL; AF257081; AAG33127.1; Ionic channel. SEQUENCE 330 AA; 36130 MW
                                                                                                                                                                                                                                                                                                            Coetzee W., Rudy "KT3.2 and KT3.3 to TASK1.";
                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence up
01-MAR-2001 (TrEMBLrel. 16, Last annotation
TWO PORE POTASSIUM CHANNEL KT3.3.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Vega-Saenz de Miera E.C.,
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                        MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERO . ROGELRARYNLSQGGYE
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                                                                                                                                                                 TLVMFQSLGERMNTFVRYLLKRIKKCCGMRNTEVSMENMVTV:FFSCMGTLCLGAAAFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANN "LIGFFSCISTLCIGAAAFSH
                                                                  LVVLRFLVASADWPERAA
                                                                                LVVLRFMTMNAEDEKRDA
                                                                                                 FEGWTFFHAYYYCFITLTTIGFGDFVALQSGEALQRKE
                                                                                                                                                                                                  MRRPSVRAAGLVLCTLCYLLVGAAVFDALESEAESGROF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVIGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIEH:
                                                                                                                                                                                                                                    167;
                                                                                                                                                                                                                                           Similarity
(TrEMBLrel.
                                                                                                                                                                                                                                    Conservative
                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    Two
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Primates;
                                                                                                                                                                                                                                                                            36130 MW;
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                                                                                                                                                                                                                                                                                                                    Novel Human
16,
                                                                  258
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        Created)
                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDF
Last sequence
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                         PRT;
                                                                                                                                                                                                                                                                                                                                                                    Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                    D.H.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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No. 9
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                                                                                                                                                                                                                                                                            :RC64;
                                                                                                                                                  FSCISTLCIGAAAFSH
                                                                                                         TILTGLTVIGAFLN
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Best Loc
Matches
                       Query Match
Best Local Similarity
Matches 172; Conserv
                                                                                                                                                                                                                                                                                                                     076795;
01-NOV-1998
                                                                                  PRINTS; PR01333
Ionic channel.
SEQUENCE 329
                                                                                                                                                                                                                                                                                      01-NOV-1998
01-MAR-2001
PUTATIVE POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-2000) to the EMBL/GenBank/DDBJ EMBL; AL118522; CAC14068.1; -. SEQUENCE 330 AA; 36222 MW; 24F428721A1C77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLre1. 16, Last annotation update)
DJ781B1.1 (A NOVEL PROTEIN SIMILAR TO THE ACID-SENSITIVE
CHANNEL PROTEIN TASK (KCNK3)).
                                                                                                   InterPro; IPR003280; -. Pfam; PF02034; TWIK_channel; 1. PRINTS; PR01333; 2POREKCHANEL.
                                                                                                                                                                Wang Z.-W., Salkoff L.; "Potassium channels in C. el Submitted (AUG-1998) to the EMBL; AF083652; AAC32863.1;
                                                                                                                                                                                                                                       Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                076795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DJ781B1
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lovel1
                                                                                                                                            InterPro; IPR001622;
                                                                                                                                                     InterPro; IPR000099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE | : | | : | | : | | : | | : | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
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MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQELRARYNLSQGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                LVVLRFMTMNAEDEKRDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLVTFQSLGERLNAVVRRLLLAAKCCLGLRWTCVSTENLVVAGLLACAATLALGAVAFSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELERVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRRPSVRAAGLVLCTLCYLLVGAAVFDALESEAESGRQRLLVQKRGALRRKFGFSAEDYR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELERLALQAEPHRAGRQWKFPGSFYFAITVITTIEYGHAAPGTDSGKVFCMFYALLGIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166;
                                                                                                                                                                                                                                                                                      POTASSIUM CHANNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FROM N.A.
                                                                                                                                                                                                                                                                                                (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 16, Last annotation updat
                                                                                                                                                                                                   Salkoff L.;
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                  ΑA;
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Primates;
                                  40.2%;
                                                                                 36992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                          258
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                                                                                                                                                                                          elegans.";
                                                                                                                                                                                                                                                    Caenorhabditis.
                        54;
                                                                                                                                                                                                                                                                                      SUBUNIT N2P38
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                      Score 820; DB
Pred. No. 1.8e
54; Mismatches
                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 838; DB 4;
Pred. No. 4.8e-66;
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                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                  338A6D9A577464CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24F428721A1C7790 CRC64;
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                       ..8e-64;
les 84;
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                                           Length 329
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                       Indels
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                       46;
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                      Gaps
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RA Wilson R., Ainscough R., Anderson K., Bayne:

RA Bonfield J., Burton J., Connell M., Copsey Coper J., Coulson A.,

RA Craxton M., Dear S., Du Z., Durbin R., Fave C., Fulton L.,

RA Gardner A., Green P., Hawkins T., Hillier I., Com., Johnston L.,

RA Jones M., Kershaw J., Kirsten J., Laister N., Atreille P.,

RA Lightning J., Lloyd C., Mcmurray A., Mortim J., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Chess D., Shownkeen R.,

RA Smaldon N., Smith A., Sonnhammer E., Stader S., Staten J.,

RA Thierry-Mieg J., Thomas K., Vaudin M., Vaud. K., Waterston R.,

RA Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.;

T elegans."
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017185
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017185;
01-JAN-1998
01-JAN-1998
01-MAR-2001
         InterPro; IPR003280; -.
Pfam; PF02034; TWIK_channel; 1
PRINTS; PR01333; 2POREKCHANEL.
                                         Submitted (SEP-1997) to the EMBL; AF025454; AAC71151.1; InterPro; IPR000099; ... InterPro; IPR001622; ...
                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
 SEQUENCE
                                                                                             SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                 Submitted
                                                                                                                                                    STRAIN-BRISTOL
                                                                                     Waterston R.;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                     Nature
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   F34D6.3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLEATIVASVELLURYLLHRAKKGLGMRRADVSMAN (3)
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                                                                                                                                                                                    368:32-38(1994).
                                                                                                                               , Wohldmann
(SEP-1997)
336 AA;
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37700
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16,
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                                                                                                                               O'Neal D.;
the EMBL/GenBank/DD:
 ₩;
                                                                          EMBL/GenBank/DDRJ
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 E0474024F69FC27E
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                     RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA George R.A., Borthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorlova B., Delcher A., Erraz C., Ferriera S., Fleischmann W.,
RA Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Havey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hashin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.
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RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,

RA Merkulov G., Milshina N.V., Murphy L., Murry D.M., Nelson D.L.,

RA Merkulov G., Milshina N.V., Murphy L., Murry D.M., Nelson D.L.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Spier E., Wassarman D.A., Weinstock G.M., Strong A.H., Wang X.,

RA Williams S.M., Woodage T., Worley K.C., Wu S., Yang S., Yao Q.A.,

RA Yel J., Yeh R.-F., Zaveri J.S., Zhan M., Zh., Shao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Rubin G.M., Venter F.,

RT "The genome sequence of Drosophila melanog. School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School School Scho
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PRINTS; PR01095; TASKCHANNEL.
                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexipoda; Insecta;
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Ephydroidea; Drosophilidae; Drosophila.
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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RA Chush B. C. Siden F. Saunders R.D.C., Scheeler F., Shen H.,

Ra Chush B. C. Siden F. Saunders R.D.C., Scheeler F., Shen H.,
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EMBL; AE003701; AAF54970.1; -. Erichons. Fign0038165; CG9637.
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S; PR01095; TASKCHANNEL.
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Pred. No. 1.8e-57
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Best Local
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O76790 PRELIMINARY; PRT; O76790; O1-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20287530; PubMed=10747866; MEDLINE=20287530; PubMed=10747866; MEDLINE=20287530; PubMed=10747866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JL57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Ve)
Mammalia; Eutheria; Rodentia; Hystricognat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003092; -.
Pfam; PF02034; TWIK_channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF212828; AAF63707.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "TASK-3, a novel tandem proe domain acid-
extracellular histidine as pH sensor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Karschin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10141;
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                                                                                                                                                                                                                                                                                                                                    96 YGHAAPSTDGGKVFCMFYALLGIPLTLVMFQSLGERIK %.
                                               15
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TQPQYVAFSEYYILTGLTYIGAFLNUVYLRFMTMNAF: (**)

TQPQYVAFSEYYILTGLTYIGAFLNUVYLRFMTMNAF: (**)

TQPQYVAFSEYYILTGLTYIGAFLNUVYLRFMTMNAF: (**)

TQPQYVAFSEYYILTGLTYIGAFLNUVYLRFMTMNAF: (**)

TQPQYVAFSEYYILTGLTYIGAFLNUVYLRFMTMNAF: (**)

TREFTYAFSTANTIVGTTYTGAFLNUVYLRFMTMNAF: (**)

TREFTYAFSTANTIVGTTYTGAFLNUVYLRFMTMNAF: (**)
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                                                                                                                                                                                                                                                                                                                                                                        163;
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53; Conservative
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HANNEL TASK3
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54.2%; Pred. No. 7.8;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PUTATIVE POTASSIUM CHANNEL SUBUNIT N2P20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003280; -.
Pfam; PF02034; TWIK_channel; 1.
Pfints; PR01333; 2POREKCHANEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998).
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the nematode C.elegans: A platform for
236 GAFLNLVVLRFMTMNAED 253
| :||:|| || ||::
243 SACVNLLVLGFMASNADE 260
                                                                                              176 AAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGLTVI 235
                                                                          183 YMFHTIEKWSIFDAYYFCMITFSTIGFGDLVPLQQVNALQDQPLYVFATIMFILIGLAVF 242
                                                                                                                                               127 MFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLTIGFMVIVS----GT 182
                                                                                                                                                                     124 MFQSLGERINTLVRYLLHRAKKGLGMR----RADVSMANMVL----IGFFSCISTLCIGA 175
                                                                                                                                                                                                                   67 AIAIKSIPQQAGYQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLFCMIFALFGVPMGLI 126
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                                                                                                                                                                                                                                        RVVLRLKPHKAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYALLGIPLTLV 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     channel
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Search completed: August 28, 2001, 17:12:47 Job time: 416 sec

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Title:
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Maximum Match 100%
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            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is proved through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as "s content is in no way modified and this statement is not removed. Using by and for commercial entities requires a license agreement (See htt://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=99254548; PubMed=10321245; Patel A.J., Honore E., Lesage F., Fink "Inhalational anesthetics activate two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fink M., Duprat
Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ЕМВО
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning, functional expression and brain levilization unconventional outward rectifier K+ channel. EMBO J. 15:6854-6862(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U73488; AAC53005.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           channels."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lazdunski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVISIONS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fonic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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  Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: INTEGRAL MEMBRANE STEIN (POTENTIAL).

TISSUE SPECIFICITY: HIGH EXPRESSION IN BELL AND LUNG. ALSO
DETECTED IN KINNEY, HEART AND SKELETAL MYSTE. NOT DETECTED IN
LIVER. IN THE BRAIN, HIGHEST EXPRESSION STACKED BULB,
HIPPOCAMPUS AND CEREBELLUM.

MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVELED BY VOLATILE GENE
ANABSTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Neurosci. 2:422-426(1999). FUNCTION: OUTWARD RECTIFYING POTASSIUM CH. : NEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISOFLURANE.
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHANNELS
MGI:109366; KcnkrPro; IPR000099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF02034; TWIK_channel;
S; PR01333; 2POREKCHANE!
                                                                                  395;
                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR003280;
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                                                                                                                                                                              95
119
411
                                                                                  Conservative
                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
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                                                                                                      97.2%;
96.1%;
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                                                                                                                                                                                      ₩.
                                                                                12;
                                                                                                                                                                                                                                                                   POTENTIAL.

PORE-FORKING (P. "WIAL).

POTENTIAL.

CYTOPLASMIC (PC: "WIAL).

ESSENTIAL FOR C: "DROFORM AS

SENSITIVITY.
                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.

CYTOPLASMIC (PC., TIAL).

COTENTIAL.

COTENTIAL.

COTENTIAL.
                                                                                                      Score
Pred.
                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
; 8F976DDD103EFA05 CRC64;
                                                                                                                                                                                                                                                 REQUIRED FOR BASAL CHANNEL ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PORE-FORMING (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ion transport; Potassium
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                                                                                  Mismatches
                                                                                                      2041;
No. 2.
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                                                                                                                       DE, i.
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ce- િાin background I
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                                                                                                                                                                                                                                                                                               HALOTHANE
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61

GATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELiQQIVAAINAGIIPLGNT

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RESULT 3
CIW4_HUMAN
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
STIMULATED POTASSIUM CHANNEL FROTEIN) (TRAAK).
                                                                                                                                                                                        This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S. "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassium channel."; Brain Res. Mol. Brain Res. 82:74-83(2000).
                                   EMBL;
                                                                                        modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 11."
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gray A.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Frontal cortex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=11042359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCNK4 OR TRAAK
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                    'Assignment of KCNK4 encoding the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
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                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the ENUTOPEAN BIOINFORMATICS. Institute. There are no restruct by non-profit institutions as long as its content
                                                                                                                                                                                                                                                           FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARD POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED EXTERNAL K+ CONCENTRATION BY SIMILARITY).
SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTE SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELTPCRRTLSVNHLTSEREVLPPLLKAESIYLNGLTPHCAGEDIAVIENMK 411
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                                     AF248242;
AF247042;
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                 18242; AAG31731.1;
17042; AAF64062.1;
IPR001622; -.
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Primates;
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                                   ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                393
                                                                                                            moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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Tons, OUTWARDLY R
                                                                                                                                                                                                                                                               FAMILY OF POTASSIUM
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                                                                                                                                                                   restrictions
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В Ş Ъ οy В Q 밁 S 밁 δÃ 밁

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RESULT 4
CIW4_MOUSE
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SUBUNIT: HOMODIMER (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND
2/TRAAKT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE.
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                                             CVLFVALPAIIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWFWI
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nannel; Transmembrane; Ion transport; Potassium transport;
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MISSING (IN ISOFORM 2).
478A834B7B7AEC92 CRC64;
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 5 (ACII (ACII VI) NSITIVE POTASSIUM CHANNEL PROTEIN TASK-2) (TWIK-RELATED ACID- (ACII VI) NSITIVE K+ CHANNEL CRUNG OR TASK2.
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J. Biol. Chem. 273:30863-30869(1998).
                                                                                                                                                                                                                                     Glycoprotein.
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MEDLINE=99030343;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
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Conservative

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01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 1 (INWARD RECTIFYING CHANNEL FOTE) (POTASSIUM CHANNEL KCNO1).
KCNK1 OR TWIK1 OR HOHO1 OR KCNO1.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                         Desir G.V., Orias M., Submitted (APR-1997)
                                                                                                                                                                                                                                                                                                                               "Sequence and function of the two P domain potassium implications of an emerging superfamily.";
J. Mol. Med. 76:13-20(1998).
                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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                                                                                                      MITCALANEOUS: INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.

SUBLITIENAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.

MISCELLANEOUS: INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.

SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
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TISSUE-Brain;
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IPR001622;
IPR001779;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                           (Mouse)
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Rodentia;
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32.5%;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -KTKEEVGEFRAHAAE
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CYTOPLASMIC (
POTENTIAL.
PORE-FORMING
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 379.5;
Pred. No. 1.
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T->A: NO EFFEC: JN CHANNEL
; 2A41D9501323215D CRC64;
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PORE-FORMING
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                                                                                                              Craniata; Vertocrata; |
Sciurognathi; Noridae;
                                                                                                                                                                                                                                                                MEMBER 1 (INWARD
                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Query Match
Best Local
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                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
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-I- FUNCTION: WEAK INWARDLY RECTIFYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arrighi I., Lesage F., Scimeca J.-C. "Structure, chromosome localization, mouse twik K+ channel gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-129/SVJ; T
MEDLINE-98218573;
                                                                                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000099; -.
InterPro; IPR001622; -.
InterPro; IPR001779; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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Lazdunski M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97165959; PubMed=9013852;
                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conic
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESION IN BRAIN,

KIDNEY, THYROID, SALLVARY GLAND, ADRENAL GLAND, PROSTATE,

EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE

EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND

OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HARART, SKELETAL

MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN

CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS CONCEPTION. EXPRESSION INCREASES FROM 2-8 DA STABILIZES AFTER DAY 8.
MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, ACIDIFICATION. ACTIVATED BY PROTEIN KINASE (SIMILARITY: BELONGS TO THE TWO PORE DOMAIN IN THE PROTECTION OF THE TWO PORE DOMAIN IN THE PROTECTION OF THE TWO PORE DOMAIN IN THE PROTECTION OF THE TWO PORE DOMAIN IN THE PROTECTION OF THE PROTECTION OF THE TWO PORE DOMAIN IN THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION
                                     FLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVA 108
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FLVLGYLLYLVFGAVVFSSEELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 channel;
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                                                                                                                                                    Similarity
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                                                                                                                    Conservative
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                                                                                                                 Score 370.5;
Pred. No. 4.9e
57; Mismatches
                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                         A996060A18266FD4 CRC64;
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c.,
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No. 4.
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DAYS AFTER BIRTH &
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACIT · 'NSITIVE POTASSIUM CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENS, IVE K+ CHANNEL).
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                                                                                  or send an
                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                   This SWISS-PROT entry is copyright. It is proposed the EMBL outstation -
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Patel A.J., Honore E., Lesage F., Fink M., Rom: G., Lazdunsk:
"Inhalational anesthetics activate two-pore-domain background
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duprat F., Lesage F., Fink M., Reyes R., Heurtenux C., Lazdunski M.; "TASK, a human background K+ channel to sense external pH variations near physiological pH.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                            InterPro;
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FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIV, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION FOR ACTS AS AN ION CONCENTRATION ON EITHER SIDE OF THE 10. BRANE. ACTS AS AN OUTWARD RECTIFICER WHEN EXTERNAL POTASSIUM "NOCENTRATION IS LOW. WHEN EXTERNAL POTASSIUM CONCENTRATION IS INWARD. SUBCELULAR LOCATION: INTEGRAL MEMBRANE ("POTENTIAL). STRONGEST TISSUE SPECIFICITY: WIDESPREAD EXPRESSIO, 37 4 ADULI, STRONGEST EXPRESSION IN PANCREAS AND PLACENTA. LOW A SYPRESSION IN BRAIN, LUNG, PROSTATE, HEART, KIDNEY, UTERUS, S. T. INTESTINE AND COLON.
                                                                                                                                                                                                                    MISCELLANEOUS: INHIBITED BY EXTERNAL AC: A HALOTHANE AND ISOFLURANE. SIMILARITY: BELONGS TO THE TWO PORE DOMA-
                                                                                                                                                                                                            CHANNELS
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J. 16:5464-5471(1997).
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                                                                                                non-profit institutions as long of scontent is in no way and this statement is not removed. We see by and for commercial requires a license agreement (See 1) 1. //www.isb-sib.ch/announce/
                                                                                                                                                           the Swiss Institute of Bioinformatid
                            IPR000099;
                                                                                  equires a license agreement (Semail to license@isb-sib.ch).
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Best Local :
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 6 (INWARD RECTIFYING POTASSIUM CHANNEL PROFEIN TWIK-2) (TWIK-ORIGINATED SIMILARITY SEQUENCE).
KCNK6 OR TWIK2 OR TOSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
SEQUENCE
                                                              MEDLINE-99285568; PubMed-10359073; Pountney D.J., Gulkarov I., Vega-Saenz de Miera E., Holmes Saganich M., Rudy B., Artman M., Coetzee W.A.; "Identification and cloning of TWIK-originated similarity (TOSS): a novel human 2-pore K+ Channel principal subunit. FEBS Lett. 450:191-196(1999).
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DOMAIN
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          Chavez
                     MEDLINE=99175162; PubMed=10075682;
                                             SEQUENCE FROM
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PRINTS; PR01333; 2POREKCHANEL.
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Pfam; PF02034; TWIK_channel;
                                                                                                                                     TISSUE=Testis;
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 z R.A., Gray A.T.,
Y., Forsayeth J.R.
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SEQUENCE
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entities requires a license agreement (See
or send an email to license@isb-sib.ch).
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EMBL; AF117708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "TWIK-2, a new weak inward rectifying potassium channel family.";
J. Biol. Chem. 274:7887-7892(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fonic channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [nterPro;
                                                                                                                                                                                                                                                             117
                                                       193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ween the Swiss Institute of Bioinform
European Bioinformatics Institute. The
by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: INTEGRAL MEMBRANE : ROTEIN (POTENTIAL)
TISSUE SPECIFICITY: WIDESPEAD EXPRESSION, DETECTED IN ALL
TESTED EXCEPT FOR SKELETAL MUSCLE. STROK: 185T EXPRESSION IN
PLACENTA, PANCREAS, HEART, COLON AND SP. 133, LOWER LEYELS DE
IN PERIPHERAL BLOOD LEUKCCYTES, LUNG, 1 74R, KIUNEY AND THYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOWEST EXPRESSION DETECTED IN BRAIN.

MISCELLANEOUS: INHIBITED BY INTERNAL AC DIFICATION AND, TO A SMALL DEGREE, BY ZINC. NOT INHIBITED BY QUINI: , OUINIDONE OR BARIUM.

SIMILARITY: BELONGS TO THE TWO PORE DOMA: N FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: HOMODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: WEAK INWARDLY RECTIFYING POTAS; SUM
                                                                                                                                                                                                                                                                                                                                         YLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAINAGIIP
                                                       AHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPY ..
                                                                          KHI-EGWSALDAIYFVVITLTTIGFGDYVAGGSDIE-Y!
                                                                                                                                                                            LLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIIST.ETLFGCVLFVA--LPAIIF
                                                                                                                                                                                                                                                        LGNTSNQIS----HWDLGSSFFFAGTVITTIGFGNISPKIEGGKIFCIIYALLGIPLFGF
                                                                                                                                                                                                                                                                                                   YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCV^APALDAFVERVLAAGRLGRVV
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                                                                                                                                      LLTASAQRLSLL - - -
                                                                                                                                                                                                                    LANASGSANASDPAWDFASALFFASTLITTVGYGYTTPL/DAGKAFSIAFALLGVPTTML
                                                                                                                                                                                                                                                                                                                                                                                  83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ); IPR001779; -.
PR01096; TWIK1CHANNEL.
hannel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h., Gray A.T., Zhao B.B., Ki
Forsayeth J.R., Yost C.S.;
them. 274:24440-24440(1999).
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AAD24000.1;
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                                                                                                                                      -LTHVPLSWLSMRWGWDPRRAACW **.VALLGVVVTVCFLVPAVIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (I POTENTIAL. PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                                                     Score 348;
Pred. No. 1
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N-LINKED (GLCNAC...) (POTENTIAL)
C->A: NO CHANNEL ACTIVITY
; 1379382DFB057 DF CRC64;
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VKPVVMEWILVGLAYFAAV 2
                                                                                                                                                                                                                                                                                                                                                                                  104;
                                                                                                                                                                                                                                                                                                                                                                                                       .6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potassium transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usaye
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RESULT
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035111; 035163;
01-CCT-2000 (Rel. 40, Created)
01-CCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
01-CCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K+ CCICARDIAC TWO-PORE BACKGROUND K+ CHANNEL) (CTBAK-1).
                                                 EMBL;
EMBL;
EMBL;
EMBL;
MGD; N
                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
                                                                                                                                                                                         use by non-profit modified and this st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Proton block and voltage gating are cardiac leak channel kcnk3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Heart;
MEDLINE-98165556; PubMed-9506712;
MEDLINE-9816556; PubMed-9506712;
MEDLINE-98165556; PubMed-9506712;
MEDLINE-98165556; PubMed-9506712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TASK, a human background "
   InterPro;
                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and functional expression background K+ channel (cTBAK-1).";
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                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20287574; PubMed=10748056; Lopes C.M., Gallagher P.G., Buck M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97459932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCNK3 OR TASK OR CTBAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem. 275:16969-16978(2000).

- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE, ACTS AS AN OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.

WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARK
                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMODIMER (POTENTIAL).

SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.

MISCELLANGOUS: INACTIVATED BY BARIUM.

SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                             AB008537; BAA25436.1;
AF006824; AAC53367.1;
AB013345; BAA28349.1;
AF241798; AAF81418.1;
AF242508; AAF81418.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (Mouse)
                                                                                                                                                                                                                              European
                                                   MGI:1100509;
                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 physiological pH.";
J. 16:5464-5471(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                round K+ channel (cTBA
Res. 82:513-518(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a human background K+
hysiological pH.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF 4-409 FROM N.A
                                  IPR000099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Rodentia;
                                                 Kcnk3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9312005;
F., Fink M., Reyes
ckground K+ channel
                                                                                                                                                                                                             institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of a novel cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   potassium-dependent
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                                                                                                                                                                                                          There are no restrictions ng as its content is in
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ndent in the
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                                                                                                                                                                                                                                             EMBL outstation
                                                                                                                                                                                                                                                          a collaboration
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Best Local
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054912;
                            MEDLINE-98099797; PubMed-9437008;
Leonoudakis D., Gray A.T., Winegar B.D., K
Taylor D.M., Chavez R.A., Forsayeth J.R.,
"An open rectifier potassium channel with
cloned from rat cerebellum.";
J. Neurosci. 18:868-877(1998).
                                                                                                                                                                                        01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 3 (ACID-SENSITIVE CHANNEL PROTEIN TASK) (TWIK-RELATED ACID-SENSITIVE K + C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
SEQUENCE
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CARBOHYD
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TRANSMEM
                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                      TISSUE=Cerebellum;
                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                KCNK3 OR TASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01095; TASKCHANNEL. PRINTS; PR01333; 2POREKCHANEL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _
         CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM ION CONCENTRATION ON EITHER SIDE OF THE HER-BRANE. ACTS
                                                                                                                                                                                                                                                                                                           QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTHN
                                                                                                                                                                                                                                                                                                                                                   MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQR#:LRQLELRARYNLSEGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNS--T
                                                                                                                                                                                                                                                                                                                              LDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKF! VGEFRAHAAEWTAN 320
                                                                                                                                                                                                                                                                                                                                                                                     FCMFYALLGIPLTLVMFQSLGERI------NTF; \LLHRAKRGLGMRHAEVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                         ELERVVLRL-KPHKAGV----
                                                                                                                                                                                                                                                                                                                                                                                                                   FCIIYALLGIPLEGELLAGVGDQLGTIFGKGIAKVEDTFI; WNVSQTK-----IRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAG: VITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF02034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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108
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244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWIK_channel;
                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                   (Rat).
                                                                                                                                                Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29
101
128
128
158
179
207
207
243
409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₩;
                                                                       Winegar B.D., Kindler Forsayeth J.R., Yost C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62;
                            VOLTAGE-INSENSITIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                       ----QWRFAGSFYFAITVITTIGYGHAAPSTDGGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC
                                                                                                                                                Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PORE-FORMING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
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V +> I (IN REF.
35236E011AACF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ion transport; F assium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343; DB 1
No. 4.1e-1
POTASSIUM CONCENTRATION
                                                                                                                                                                                                                                                         411
                                                                                                                                                                                                                                                         ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Pr LELLIAL)
                                                             CV0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (I YIN ATIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                      :-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 1;
16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2);
87
                                                             pore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 409;
                                                                       C.H.,
                              BACKGROUND
                                                             domains
                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
                                                                                                                                                Murinae;
                                                                                                                                                                                           CHANNEL).
                                                                                  Harada
                                                                                                                                                                                                     POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transport;
                  POTASSIUM
         AS AN
                                                             İn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
                              POTASSIUM
                                                             tandem
                                                                                                                                                 Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
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ORK1_DROME
ID ORK1_D
AC Q94526
DT 01-OCT
DT 01-OCT
                                                                                        RESULT
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Best Local S
Matches 88
   ORK1_DROME
Q94526;
Q1-OCT-2000
Q1-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1095; TASKCHANNEL.
PRINTS; PRO1333; 2POREKCHANEL.
Ionic channel; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF031384; AAC39952.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000099;
                                                                                                                                                                             267
                                                                                                                                                                                                              157
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                                                                                                                                           217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODDERATE
EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AND
SKELETAL MUSCLE.
SKELETAL MUSCLE.
MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC
BUPIVACAINE AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A.
SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIU
CHANNELS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European
                                                                                                                                           QPQYVAFSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-AEHRALLTHN
                                                                                                                                                                        LDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTAN
                                                                                                                                                                                                                                MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLELRARYNLSEGGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKWKTVSTIFLVV--VLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNS--T 97
                                                                                                                                                                                                              ANMVLIGFVSCISTLCIGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQT
                                                                                                                                                                                                                                                                               FCMFYALLGIPLTLVMFQSLGERI---
                                                                                                                                                                                                                                                                                                                 FCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTK-----IRI
                                                                                                                                                                                                                                                                                                                                                    ELERVVLRL-KPHKAGV--
                                                                                                                                                                                                                                                                                                                                                                                    ELDELIQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Swiss Institute of Bioinformatics and the EMBL outstation opean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way dand this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR003280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
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   (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AΑ;
                                                      STANDARD;
   40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.3%;
29.9%;
                   Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
PORE FORMING (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PORE-FORMING (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 343; DB 1;
Pred. No. 4.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ion
                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LINKED (GLCNAC...) (P
D2778016E09E2BF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                 ----NTFVRYLLHRAKRGLGMRHAEVSM
                                                                                                                                                                                                                                                                                                                                                  -QWRFAGSFYFAITVITTIGYGHAAPSTDGGKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transport; Potassium
                                                        1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                           267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZINC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RA Adams N.D., Celniker S.E., Holt R.A., Evans ..., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Honderson S.N.,
RA George R.A., Levis S.E., Richards S., Ashburro, M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zha, S., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zha, S., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Bayraki, S., Koch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraki, S., W., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Bayraki, S., W., Cher A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadleu F., Cher A., Chandra I.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandui D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandui D., Bolshakov S.,
RA Glory J.M., Cawley S., Dahlke C., Davenpor,
RA Gerbis M., Delcher A., Deng Z., Mays A.D., S., Fleischman W.,
RA Cherry J.M., Cawley S., Dahlke C., Davenpor,
RA Gerbis M., Delcher A., Deng Z., Mays A.D., S., Fleischman W.,
RA Colos R., Congelista C.C., Ferraz C., Fr. C. C., S., Fleischman W.,
RA Dodson K., Doup L.E., Downes M., Dugan-Roch., Davles P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Roch., Dankov B.C., Dunn P.,
RA Dodson K., Bouterialian A.E., Garg N.S., Gelbb. W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernanid, R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernanid, R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravit. R., Houck J.,
RA Glodek A., Gong F., Karpen G.H., Ke Z., K., S., Houck J.,
RA Glodek A., Gong F., Karpen G.H., Ke Z., K., S., Houck J.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.I., Vepherson D.L.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravit. R., Houck J.,
RA Merkulov G., Milshina N.V., Mobarry C., Mori. J., Noshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Mori. J., Noshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Mori. J., Noshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Mori. J., Noshrefi A.,
RA H., Shan M., Welson K.A., Nixon K., Nixola 
                                                                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; ハンジ・コda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; ...chycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHANNEL ORK1).
ORK1 OR CG1615.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97075152; PubMed-8917578; Goldstein S.A.N., Price L.A., Rosenthal D.N. Portassium-selective leak channel v. cloned from Drosophila melanogaster by expressioned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPEN
                                                                                                                     STRAIN-BERNELDI,
MEDLINE-20196006; PubMed-10731132;
MEDLINE-20196006; PubMed-10731132;
Medline-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cerevisiae."
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MISCELLANEOUS:
SIMILARITY: BE
                                                                                SUBCELLULAR LOCATION: INTEGRAL TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN MUSCLE, BRAIN AND
                                                                                                                                                                                                     FUNCTION: BACKGROUND POTASSIUM CHANNEL. FO'LIFICATION IS DEPENDENT ON EXTERNAL POTASSIUM CONCENTRATION. ACTS 7.5 AN OUTWARDLY RECTIFYING CHANNEL BUT AS EXTERNAL POTASSIUM LEVELS INCREASE, THIS
                                                             IN LARVA AND
                                                                                                                                                                             IS REVERSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CT-2000 (Rel. 40, Last annotation update).
RECTIFIER POTASSIUM CHANNEL PROTEIN 1 (7.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N.A.
JS: INHIBITED BY BELONGS TO THE T
   Y BARIUM.
TWO PORE
                                                                                         AND
                                                                                      L MEMBRANE PROFE
D EXPRESSION IN .
ND OVARY ALSO P
      DOMA ; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - 1000 July 1
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                                                                                                                                                 PRO. EIN (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wo pore domains in Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                         PRESENT
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      AMILY
      QF.
                                                                                      STRONGEST
AT LOW LEV
      POTASSIUM
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
POTASSIUM CHANNEL SUBFAMILY K MEMBER 8 (PUTATIVE POTASSIUM CHANNEL DP3) (DOUBLE-PORE K+ CHANNEL 3) (NEUROMUSCULAR TWO P DOMAIN POTASS:
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
                                            Mus musculus (Mouse)
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an email to license@isb-sib.ch).
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EMBL; AF110521; AAD29577.1;
EMBL; AB015729; BAA35074.1;
EMBL; AF022820; AAD09337.1;
EMBL; AF012324; AAF21603.1;
EMBL; AF158234; AAF14528.1;
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                        TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lazdunski
                                                                                                                                                                                                                                                                                                             SUBUNIT: HOMODIMER (POTENTIAL).
TISSUE SPECIFICITY: DETECTED IN EMBRYO, TYL LUNG AND LIVER.
WEAKLY EXPRESSED IN COLON, TESTIS, ATRIA. NUMBY, INTESTINE,
BLADDER, UTERUS, OVARY, SALIVARY GLAND, HAVING AND BRAIN STEM.
DETECTED IN BRAIN, CEREBELLUM, SPINAL CONT. 4EART, VENTRICLE,
SKELETAL MUSCLE, LIVER, PLACEMTA AND DANIMALS. IN THE EXE, HIGH
EXPRESSED IN THE RETINAL GANGLION CELL LAYER AND INNER NUCLEAR
                                                                                                                                                                                                                                                                              SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PROBABLE POTASSIUM CHANNEL SUBJUJ: NO CHANNEL ACTIVOBSERVED IN VITRO AS PROTEIN REMAINS IN THE ENDOPLASMIC RETICUMAY NEED TO ASSOCIATE WITH AN AS YET UNKNOWN PARTNER IN ORDER REACH THE PLASMA MEMBRANE.
                                                                                                    MGI:1341841; Kcnk8
                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is provered through sen the Swiss Institute of Bioinformatic: and the EN
                                                                  ); IPR003280; -.
PR01333; 2POREKCHANEL.
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                                                                                                                                                                                                        non-profit institutions as long and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           localization, channel KCNK6
                                                                                        IPR001622; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SEP-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JUN-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                  equires a license agreement (See http://www.isb-sib.ch/announce, email to license@isb-sib.ch).
1
11
92
120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buck M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a unique pore structure.";
274:11751-11760(1999).
                                                         Transmembrane;
                                                                                                                                                                                                                                                                                        BELONGS
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R., Lesage F., F
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10
31
118
140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and expression
                                                                                                                                                                                                                                                                                        TO THE TWO PORE DOMAIN ! AMILY OF POTASSIUM
                                                                                                                                                            ALT_TERM
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                                 CYTOPLASMIC
            PORE-FORMING
                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              channel subfamil;
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                                                        Ion transport;
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                                                         transport;
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                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
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Best Local Similarity
Matches 82; Conser
      homologue with a unique pore structure.";

J. Biol. Chem. 274:11751-11760(1999).

-!- FUNCTION: PROBABLE POTASSIUM CHANNEL SUF
OBSERVED IN VITRO AS PROTEIN REMAINS IN
MAY NEED TO ASSOCIATE WITH AN AS YET UNK
REACH THE PLASMA MEMBRANE.
-!- SUBULT: HOMODIMER (POTENTIAL).
-!- SUBULTI HOMODIMER (POTENTIAL).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHC
PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: BELONGS TO THE TWO PORE DOMA
CHANNELS.
                                                                                                                                                                                                                                                                                                        V7_HUMAN S'
CIW7_HUMAN S'
Q9Y2U2; Q9Y2U4; (
01-OCT-2000 (Rel
01-OCT-2000 (Rel
01-OCT-2000 (Rel
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TRANSMEM
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                                                                                                                                                                           Salinas
                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                             POTASSIUM CHANNEL SUBFAMILY K MEMBER
                                                                                                                                                  "Cloning of a new mouse two-P domain channel
                                                                                                                                                               Lazdunski M.;
                                                                                                                                                                                     MEDLINE-99223496; PubMed-10206991;
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALLGIPLFGFLLAGVGDQLGTIF---GKGIAKVEDTFIKWNVSQTKIRIISTI-IFILFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IQQIVAAINAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGQFALLGYLLLGL----
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173
199
233
254
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293
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(Rel. 40, Last sequence up)
(Rel. 40, Last annotation)
                                                                                                                                                                         Reyes R.,
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                    HOMODIMER (POTENTIAL).

LIAR LOCATION: INTEGRAL MEMBRANE PROTEIN
IYE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE)
BY ALTERNARIVE SPLICING.

TY: BELONGS TO THE TWO PORE DOMAIN FAMIL
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193
227
253
307
83
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232
293
32168
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                                                                                                                                                                                                                                             Chordata;
Primates;
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28.98;
                                                                                                                                                                        Lesage F., Fosset M., Heurteaux C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
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MGS -> TR (IN REF. 4).
GS -> THSREFGPRGOEFGTR (IN R)
GS -> THSREFGPRGOEFGTR (IN R)
G -> S (IN REF. 2, 3, 4 AND 1
YH -> SP (IN REF. 2).
T -> P (IN REF. 2).
YH -> SP (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PORE-FORMING (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 296.5; DB 1;
Pred. No. 3.8e-13;
7; Mismatches 94;
                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                -LAVETFSELPQVRA
                    PORE DOMAIN FAMILY
                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                      307
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                                                                                         SUBUNIT: NO CHANNEL ACTIVITY IN THE ENDOPLASMIC RETICULUM UNKNOWN PARTNER IN ORDER TO
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                                                      (POTENTIAL)
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                    POTASSIUM
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RESULT
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Best Local S
Matches 85
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EMBL; AF110524;
EMBL; AF110523;
                                                                                                                               _CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
CARBOHYD
Rhabditidae, pelioderinae, NCBI_TaxID=6239, [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is proved through a collaboration between the Swiss Institute of Bioinformat. and the EMBL outstation the European Bioinformatics Institute. The type no restrictions on its use by non-profit institutions as long as the content is in no way modified and this statement is not removed. Fige by and for commercial
                                          Caenorhabditis elegans
                                                      TWK-8 PROTEIN.
TWK-8 OR F22B7.7
                                                                                                P34410;
01-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 603940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See l. \cdots : //www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                 Eukaryota; Metazoa; Nematoda; Chromadorea; R
                                                                           01-FEB-1994
15-JUL-1998
                                                                                                                     TWK8_CAEEL
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                                                                                                                                                                                                                                                                                                       67
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                                                                                                                                                                        ALLGYLLLGL-----LAML-----LAVETFSELPQVFAR::KFFRPSGPVTAE
                                                                                                                                                                                     ----WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEF:
                                                                                                                                                                                                                                    VALPAIIFKHIEG-WSALDAIYFVVITLTTIGFGDYVAC
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                                                                                                                                                                                                                                                                                                       LGTALATQAHGVSTLGNSSEGRT-WDLPSALLFAASILT (TGYGHMAPLSPGGKAFCMVY
                                                                                                                                                                                                                                                                                                                  WSRYGLLVVAHLLALGLGAVVFQALEGPPACRLQAELRALLAAFQAEHRACLPPGALEEL
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307
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(Rel.
(Rel.
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; AAD29580.1;
; AAD29579.1;
                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            307 P
31946 MW;
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257
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                                                                           Last sequence u
Last annotation
                                                                                                Created)
                       Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            splicing.
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                                                                                                                                                                                                                                                                                                                                                                                         Score 291.5; DB ]
Pred. No. 8.2e-13;
3; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CYTOPLASMIC
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISSING
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N-LINKED (GLCNAC. . .) (POTENTIAL)
YLLLGLLAMLLA -> GGTSLQGTAWEG (IN I
                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN ISCEDEN BD4A36DD9591ADAC C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PORE-FORMING POTENTIAL.
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PORE-FORMING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porassium
                                                                                                                                                                                                                                                                                                                                                                                          111;
                                                                    4
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                                                                                                                                                                                                                                      COLEYLDFYKPVVWF----
                                 'drtida;
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                                                                                                                                                                                                                                                            AALLQAVALGLLVASSF
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                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                  Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transport;
                                                                                                                                                                                                                   -PVIYHLGQL
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                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                  222
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335 AA; 38472 MW; 27DE7F1E79B3CA29 CRC64;
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